

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 00:16:37 ; Search time 10533 Seconds
(without alignments)
11252.122 Million cell updates/sec

Title: US-10-782-570-3
Perfect score: 2085
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vi.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2085	100.0	2085	6	CQ868309	CQ868309 Sequence
2	2085	100.0	2235	6	CQ868307	CQ868307 Sequence
3	1794.4	86.1	2208	6	CQ868305	CQ868305 Sequence
4	334.6	16.0	3543	1	BTTOXD1	Y00423 Bacillus th
5	334.6	16.0	4253	1	BACISRH4	D02048 Bacillus th
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ALIGNMENTS

RESULT 1	CQ868309	Sequence 10 from Patent WO2004074462.	2085 bp	DNA	linear	PAT 13-SEP-2004
LOCUS	CQ868309	Sequence 10 from Patent WO2004074462.				
DEFINITION	CQ868309	Sequence 10 from Patent WO2004074462.				
ACCESSION	CQ868309	Sequence 10 from Patent WO2004074462.				
VERSION	CQ868309.1	GI:51998355				
KEYWORDS	Bacillus thuringiensis					
SOURCE	Bacillus thuringiensis					
ORGANISM	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.					
REFERENCE	1	Carozzi, N., Hargiss, T., Koziel, M.G., Duck, N.B. and Carr, B.				
AUTHORS		Delta-endotoxin genes and methods for their use				
TITLE		Patent: WO 2004074462-A 10 02-SEP-2004;				
JOURNAL		Athenix Corporation (US)				
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ORIGIN

Query Match 100.0%; Score 2085; DB 6; Length 2085;									
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Matches 2085; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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RESULT 4
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
PUBMED
AUTHORS
JOURNAL
COMMENT
FEATURES
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BTTOXD1
Bacillus thuringiensis gene for 130 kDa delta-endotoxin.
Y00423
Y00423.1 GI:40351
delta-endotoxin; endotoxin.
Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
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Ward,E.S. and Ellar,D.J.
Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene encoding a 130 kDa delta-endotoxin
Nucleic Acids Res. 15 (17), 7195 (1987)
2821500
2 (bases 1 to 3543)
Ward,E.S.
Direct Submission
Submitted (11-MAY-1987) Ward E.S., University of Cambridge, Department of Biochemistry, University of Capbridge, Tennis Court Rd., Cambridge CB2 1QW
*strain= var.israelensis;
Data kindly reviewed (12-JAN-1988) by Ward E.S.
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DB	841	AGTAATCTTTGATGGAATATAAATCTGGAACACATACATACTGATCGAACAAAAATGACT	900
QY	799	ATCGCTCAATTTTCTTTTATGATATATAAGAGATACAAAGATCAATAGNAGAAATAGGT	858
DB	901	ACTGCTGATTAGATGTTGTGCACTTTCCTTAATATGATGATAGTAAATATCCAAAT	960
QY	859	GGCAATTAACCTGAACCTTACAGAGAAATTTATCAAACTGAAATAAATTTTGACCGTCT	918
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QY	919	ACTTACCTTGAATTTCAACCAATCTCGCTATTAATGGAATATTAATTTAACACGTTCCAGG	978
DB	1014	AAGCCCTATAAATATTATGACTTTCAATATCAAGAGGATTCATTTACAGTACGACCGCA	1073
QY	979	CTTATGATTTATTTTCAATTTTATGATGAATTTATTTATACAAAAATGAAAGTACGGG	1038
DB	1074	TTTATTTACTTGGCTGATCTTTGAAATTTTATGAAAGGCGCAAACTACTCTTAATAA	1133
QY	1039	AATCGTTTGTGTTATGCGAATCGTAATPAGATCTACTTT-ATGCTACGACAGGAACCTGA	1097
DB	1134	TTTTTTCACCGCCATTTAATAATGTTTCATTACACACTTGATAATATATCCAAAAATC	1193
QY	1098	AATTATATGGAAGAAGACAGGTCACCCACACAAAACTTTTAATACCATTTGGAATC	1157
DB	1194	TAGTGTTTTGGAAATCCAAATGTAACCTGATAAAATTTAAATCTCTTTGGTTGGCAACAA	1253
QY	1158	CTATAAGTTTCAATTTGTAAGTATAGACAAAGTAACTCTCTACTTCCCTTTTCTTAACAT	1217
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DB	1314	TAATATTAGTAAATGGATTTTTTTTATACTAATAGTACTAGACTTTTGGAGAAGAACT	1373
QY	1278	ATATTACGCTGGGGGAATTTATCTAATGATAAAAAACAACTGATTTTCAATTTCCCTGT	1337
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QY	1338	AAAAAAGACTGTAAACCAATTTAATCCAAATTTGTTTACCAGCTATAATAGTTATAG	1397
DB	1434	TCCTAAACGAGAGAAATCAAGAAACCTTACCCTTTTCCACATATGATACTATAG	1493
QY	1398	TCATATTTTATCCAGTTTCTTTTATTTATTTATTTCTTATAAATTTGGATTTAGCGCTAA	1457
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QY	1518	ATCAGATAAAATAATTTACAATGATCCAGCAATCAAAGTAAACAGTCTTTGATACAAACTC	1577
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RESULT 5		BACISR4	
LOCUS		4253 bp DNA linear BCT 17-FEB-1998	
DEFINITION		Bacillus thuringiensis israelensis plasmid gene for 130 kDa	
ACCESSION		D00248	
VERSION		D00248.1 GI:216289	
KEYWORDS		130 kDa insecticidal protein (ISR4).	
SOURCE		Bacillus thuringiensis serovar israelensis	
ORGANISM		Bacillus thuringiensis serovar israelensis	
REFERENCE		1 (bases 1 to 4253)	
AUTHORS		Sen, K., Honda, G., Koyama, N., Nishida, M., Neki, A., Sakai, H.,	
TITLE		Cloning and nucleotide sequences of the two 130 kDa insecticidal	
JOURNAL		protein genes of Bacillus thuringiensis var. israelensis	
COMMENT		Agric. Biol. Chem. 52, 873-878 (1988)	
FEATURES		The genes of ISR3 and ISR4 that were 130 kDa insecticidal	
source		protein genes. ISR3 and ISR4 were identical and compared with other insecticidal	
Location/Qualifiers		C-terminal 467 amino acids.	
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ORIGIN
Query Match 16.08; Score 334.6; DB 1; Length 4253;
Best Local Similarity 53.98; Pred. No. 4.5e-36;
Matches 858; Conservative 0; Mismatches 695; Indels 38; Gaps 7;
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RESULT 6	I08083	4451 bp	DNA	linear	PAT 02-DEC-1994
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DEFINITION	I08083				
ACCESSION	I08083				
VERSION	I08083.1	GI:589204			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 4451)				
AUTHORS	Ellar, D.J. and Ward, E.S.				
TITLE	New toxin-encoding DNA fragments from <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i>				
JOURNAL	Patent: EP 0296870-A1 1 28-DEC-1988;				
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AUTHORS Ellar,D.J. and Ward,E.S.
JOURNAL Patent: WO 8810305-A 1 29-DEC-1988;
FEATURES Location/Qualifiers
source 1. .4451
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ORIGIN

Query Match 16.0%; Score 334.6; DB 6; Length 4451;
Best Local Similarity 53.9%; Pred. No. 4.4e-36;
Matches 858; Conservative 0; Mismatches 695; Indels 38; Gaps 7;
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QY 2055 TATAGAGCCACAACTATCATTTGATTAA 2085
DB 3020 ATCAGAACTTACAGATTATGACATAGATCAA 3050

RESULT 8

E01676 LOCUS 4934 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA sequence encoding Bacillus thuringiensis insectivorous protein.
ACCESSION E01676
VERSION E01676.1 GI:2169929
KEYWORDS JP 1988230090-A/1.
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 (bases 1 to 4934)
AUTHORS Komano, T. and Himeno, M.
TITLE INSECTICIDAL PROTEIN OF STRAIN BACILLUS THURINGIENSIS VAR
JOURNAL Patent: JP 1988230090-A 1 26-SEP-1988;
COMMENT OS Bacillus thuringiensis
PN JP 1988230090-A/1
PD 26-SEP-1988
PF 19-MAR-1987 JP 1987066844
PI KOMANO TORU, HIMENO MICHIO
PC C12N1/00, A01N63/00, C12N1/20, C12P21/02, C12N1/02, (C12N1/20,
PC C12R1:19);
CC strandedness: Double;
CC topology: Linear;

12324359
 2 (bases 1 to 127923)
 REFERENCE
 AUTHORS Parkhill, J.
 TITLE Direct Submission
 JOURNAL Submitted (19-APR-2002) Submitted on behalf of the pBtoxis
 sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
 Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
 COMMENT
 Details of pBtoxis sequencing at the Sanger Centre are available on
 the World Wide Web.
 (URL, http://www.sanger.ac.uk/Projects/B_thuringiensis/).
 FEATURES
 source
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 3090. 3106
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 Bh364 protein TR:Q9KAC5 (EMBL:AF001515) (378 aa) fasta
 scores: E(): 1.6e-16, 35.45% id in 189 aa, and weakly to
 Lactobacillus delbrueckii integrase/recombinase orf2
 TR:Q48538 (EMBL:Z50864) (333 aa) fasta scores: E(): 6.3,
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 scores: E(): 8.5, 23.88% id in 180 aa"
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misc_feature

RBS

gene

CDS


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Qy      2055 TATAGAGCCACAAACTATGATATTGATTA 2085
Db      94399 ATCAGAACTTACAGATTATGACATAGATCAA 94369

RESULT 10
BTH251977
LOCUS   BTH251977
DEFINITION Bacillus thuringiensis subsp. medellin cry29Aa gene for Cry29Aa protein.
ACCESSION AJ251977
VERSION   1
KEYWORDS  cry29Aa gene; Cry29Aa protein.
SOURCE    Bacillus thuringiensis serovar medellin
ORGANISM  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
1 Delecluse, A. and Orduz, S.
  Characterization of two new mosquitocidal toxins, Cry29A and Cry30A, from Bacillus thuringiensis medellin
  Unpublished
2 (bases 1 to 6009)
Delecluse, A.
  Direct Submission
  Submitted (22-DEC-1999) Delecluse A., Bacteries & Champignons Entomopathogenes, Institut Pasteur, 25, rue du Dr Roux, 75724 Paris Cedex 15, FRANCE
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Query Match      10.6%; Score 221.8; DB 1; Length 6009;
Best Local Similarity 65.2%; Fred. No. 6e-21;
Matches 376; Conservative 0; Mismatches 192; Indels 9; Gaps 3;

Qy      1473 TGCATTAGATGGACACAGTAGTGTGTTAATAGAAATAATGCAATATATCAGATAAAATAAT 1532
Db      2027 TCTTTTGCATGGACATCTACTACAAATTCCTTGAATAATGAATAAAATGATATTAT 2086

1533 TACAATGATCCAGCAATCAAGGTAAACAGTCTTGTATACAAAACCTCTTAAGGTAAATTCGAAGG 1592
2087 CACAAAATCCCTGCTGTATAAAGCCCTATCAATTTAGGTGTGCAATCAACAAGTGAATTAAGG 2146
1593 ACTGTGTATACAGAGGAGAACTTGTGTTATTTTACAAGTCAAGGCGGTTAGAGATTAC 1652
2147 TCCAGGTCTACTGTGTGGAGACTTAAATAAATTTAAATCAAAATGATTTATTTAGGTATATC 2206
1653 ATGTAGA---ACTCCCTAAATCTTACACAATCTTATTACATTTAGACTTCGATACGCTACAA 1709
2207 ATGTCAACACTTATCTAATGTTACAAAAAATATTTTGTAAAGATTCGCTACGCTACAA 2266
1710 TGGTGTCTGGAATPACTCTTCTTAATATATCTCTTACAATACCAAGGAGTAAATAGAAATACC 1769
2267 TGGTCTCTTAATATCTAGGCCCATTAATAATATTACAATTTCCAGG---AATGACACCACA 2323
1770 ACCTCAACACTCAACAACACTTTTCTGGTACAAATTAATAATTTACAATACCGAGA 1829
2324 AGGTATGGTACTCGATAAATACCTTTTCTGGTACAGGTATAGCAATTTAGAAATATCAAA 2383
1830 TTTTGGGTATTTCCAAATTTCCAGGTACAGTAACATTACCTTTTAAATCGAAACATACCATT 1889
2384 TTTTGGCTATAAAGAATTTCTAAAGAGGTAACTTAATCCAAATCAAAGTATATCTCT 2443
1890 TATATTTAATCGTGCAGATGTA---TCAAATTCAAATTTTAAATCATTTGATATAAATTTGAAT 1946
2444 TACATTAATCGTTCGTGATCAAAATTCAAATTCAAATTTTCTCTCTGATAGAATTTGAAT 2503
1947 TATACCAATTAATCTCTCTGTCGACCAAAATAGAGAAAACAAAATTTAGAAATATCCCA 2006
2504 TCTACCAATTAATCTCTCTATACGAAAAGTAAAGAACAAACAAAATTTAGAAAAAATCA 2563
2007 AACAAAAATAAATACATTTTTCACAAATCATACAAA 2043
2564 GAAACGCTAAACAAGTTATTTTCAATTAATAATAA 2600

RESULT 11
DQ078744
LOCUS   DQ078744
DEFINITION Bacillus thuringiensis strain LDC-9 cry4A insecticidal protein (cry4A) gene, partial cds.
ACCESSION DQ078744
VERSION   1
KEYWORDS  DQ078744.1 GI:68348788
SOURCE    Bacillus thuringiensis
ORGANISM  Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
1 (bases 1 to 434)
Mahalakshmi, A., Sujatha, K. and Shenbagarathai, R.
  PCR analysis and molecular characterization of cry4A gene of indigenous Bacillus thuringiensis LDC-9
  Unpublished
2 (bases 1 to 434)
Mahalakshmi, A., Sujatha, K. and Shenbagarathai, R.
  Direct Submission
  Submitted (31-MAY-2005) PG Department of Zoology and Research Centre, Lady Doak College, Chinnachockikulam, Madurai, Tamilnadu 625002, India
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Query Match      10.6%; Score 221.8; DB 1; Length 6009;
Best Local Similarity 65.2%; Fred. No. 6e-21;
Matches 376; Conservative 0; Mismatches 192; Indels 9; Gaps 3;

Qy      1473 TGCATTAGATGGACACAGTAGTGTGTTAATAGAAATAATGCAATATATCAGATAAAATAAT 1532
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810 TTCTTTTATGATTAAGAGATACAAAGATTCNAATAGGAGAAATAGGTGCGCATTAAGAAC 869
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870 TGAACCTTACAAGAGAAATTTATACAACTGAATAAATTTTGACCGTCTTACTTTACCTTGA 929
1949 AGAATTAACAGAGAGGTTTATACAGTTTATACAGTTTATAGATCCACCTGGTTTAAATGCTGGCCAA 2008
930 AATTCAACCCAACTCTCGCTATAATGGAATATAATTTAAACAGTTTCAGGGCTTATGATTTAT 989
2009 ACCAGAAATAGATTTTCAAGTTTATTTGGAAGATCATTTTAAACAGACCA---CCAGGGCTATT 2065
990 TTTCAATTTTATGATGAACTTATTTTATACAAAATTAAGAACTGACGGGAATCGTTTAGT 1049
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2170 CGATGAAATATTTATGTTAATACAAATAGATTAAGTAAGCAGCTCATTTACATTTATAC 2229
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1950 ACCAATTAATCTCTCTGTACGCCAAATATAGAGAAACAAACAAATTTAGAACTATCCAAAC 2009
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RESULT 13
ABI25059
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VERSION
KEYWORDS
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REFERENCE
AUTHORS
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JOURNAL
REFERENCE
AUTHORS
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JOURNAL
FEATURES
source

ABI25059 3752 bp DNA linear BCT 28-OCT-2003
Bacillus thuringiensis serovar entomocidus cry30Aa like gene for
putative mosquitocidal toxin and hypothetical protein gene,
complete cds.
ABI25059 GI:37999233
Bacillus thuringiensis serovar entomocidus
Bacillus thuringiensis serovar entomocidus
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.

1
Ikeya, T., Yamaya, K., Ito, T., Sahara, K., Bando, H. and Asano, S.
Cloning and Expression of Novel Crystall Protein Genes from Bacillus
thuringiensis subsp. entomocidus INA288
Unpublished
2 (bases 1 to 3752)
Ikeya, T., Yamaya, K., Ito, T., Sahara, K., Asano, S. and Bando, H.
Direct Submission
Submitted (24-OCT-2003) Tomonori Ikeya, Graduate School of
Agriculture, Hokkaido University, Department of Applied Bioscience,
Kita-9-jo, Nishi-9-chome, Kita-ku, Sapporo, Hokkaido 0608589, Japan
(E-mail: ikeyan@ab.s.agr.hokudai.ac.jp, Tel: 81-011-706-2487 (ex.2487),
Fax: 81-011-706-2487)

Location/Qualifiers
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ORIGIN

Query Match 8.7%; Score 180.4; DB 1; Length 3752;
Best Local Similarity 49.6%; Pred. No. 2.7e-15;
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DB 587 ATAAACCGCATTTATAAATCTTTATGCAAACTGCTAATATTGATTTGATTTATATC 646
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DB 647 AAAGAGGGCGTATATGAGATGATTTGGGAAAAGATATAAATGGATC-----TATAT 700
QY 620 CTAACTGCTGAACATCAGATGACTATTATAAATCTTTTAAAGAAATATACCTTAATATA 679
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QY 920 CTTTACCTTGAATTTCAACCCAACTCTCGCTATAATATGAATATAATTTAAACAGCTTCAGGGC 979
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QY 1160 ATAAAGTTTCAATTTGTAATGATAGACAACTACTCTACTTCCCTTCTTCTTAACATAT 1219

DB 1229 ATAAATTAATCAATGTCACAAATATCATCATCCAAATGATTGTAGCTCAATAGCTGGATTT 1288
QY 1220 ACTTTTCAATTAATCAAAATTTGAACCTTTATTTAAATAATTTCACTAGTAAATAAATTAACAT 1279
DB 1289 CGGATATGACCTTTTATAAAAGTGATTATAATGTTAAATGTCATCGGCAACTCA---AACTT 1345
QY 1280 ATTGAGCTGGGGGAATTTTATCTAATGATAAAACAACTGATTTTCAATTTCCCTGTAA 1339
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QY 1340 AAAAGACTGTAAACCAATTTATTAATCCAAATTTGTTTACCAAGCTATAATAGTTATAGTC 1399
DB 1400 AAAAGACTCAAGCTCAATATATTTCCATTAACAAACAAAGCATATATCTATCTGATA 1459
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QY 1820 AATACGGAGATTTTGGGTATTTCCAAATTTCCAAAGTACAGTAACNTTACCTTTAAATCGAA 1879
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QY 1880 ACATACCAATTTATATTTAATCGTCAGATGTATCAAAATTTCAATTTTAAATCATTTGATAAAA 1939
DB 1895 GTATAGATGATGATATAGAGGTGTACAAATGATCGCAATGATATATGATAGATAGAA 1954
QY 1940 TTGAATTTATACCAATTTACTTCTCTGACGCCAAATAGAGAAACAAAATTTAGAAA 1999
DB 1955 TTGAATTTCTTCCAATAACTCAATCTGTATTAGATTATACAGAGGAACAAAACATAGAAA 2014
QY 2000 CTATCCAAACAAAATAAATACATTTTTCACAAATCATACAAA 2043
DB 2015 AATCAGAGAAAGCGGTGAATGATGACCTTTTATCAATTTAAACAAA 2058

RESULT 14

ABI93814
LOCUS
DEFINITION
Bacillus thuringiensis gene for Cry30-like, hypothetical protein,
complete cds.
ACCESSION
ABI93814
VERSION
ABI93814.1
KEYWORDS
GI:54695304
SOURCE
Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
REFERENCE
1

ABI93814 3642 bp DNA linear BCT 28-OCT-2004
Bacillus thuringiensis gene for Cry30-like, hypothetical protein,
complete cds.

ACCESSION
ABI93814
VERSION
ABI93814.1
KEYWORDS
GI:54695304

SOURCE
Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.

REFERENCE

1

Ohgushi, A., Wasano, N., Saitoh, H. and Ohba, M.
Identification and characterization of novel cry genes from an
mosquito-specific *Bacillus thuringiensis* serovar sotto strain
Unpublished
2 (bases 1 to 3642)
Ohgushi, A., Wasano, N., Saitoh, H. and Ohba, M.
Direct Submission
Submitted (26-OCT-2004) Akira Ohgushi, Kyushu University, Graduate
School of Agriculture, 6-10-1, Hakozaki, Higashi-ku, Fukuoka,
Fukuoka, 812-8581, Japan (E-mail: ohgushi@bbs.kyushu-u.ac.jp.
Tel: 81-92-642-3028, Fax: 81-92-642-3028)

FEATURES
source
1. 3642
/organism="Bacillus thuringiensis"
/mol_type="Genomic DNA"
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ORIGIN
Query Match 8.2%; Score 170; DB 1; Length 3642;
Best Local Similarity 49.7%; Pred. No. 6.8e-14;
Matches 828; Conservative 0; Mismatches 750; Indels 88; Gaps 12;
419 CTCCTTGACTCTTAAATACGATTTGAGAAATGTTCCAAATGATTTTATTCAGAAATAC 478
503 CTCAGTAGCTGTATACAAATGATTTTTCAGTGTAGGATCAATCATTCGACTTTAAG 562
479 CTGGTTCCTCAACTGAACT---TATAAAGCGTATTACTACTATTATGCGCAAGCTG 535
563 ATCGCTTCTTAAATTCCTGAAATTAACCTGCATTTCTAATTTCTATGACAAACTG 622
536 CTAATTTTCAATTTAAATTTATTAACAAGGCTGCTGAATTTGGCTGATGAATGCAATG 595
623 CCAATTTTGATTTGATTTTATATCAAGAGGGGCTTTATATGACAGATGAATGCGAAATG 682

QY 596 ATATACATCCTTTCACAAATTTGAACCTTAATGCTGGAAACATCAGATGACTTATTATAACTTT 651
DB 683 ATATAAATAGATCTATATCTCCATCTTTGGGT-----TCAAAGAGACTATTATATATCTT 736
QY 656 TAAAGAAATATATACCTTAATATAGTAACTATTGTGCAAAATACCTATAGAGAGACTAA 715
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QY 716 ATAACTTCGAAACGAACCTTAATATGAGATGAGATATATTAACTGATTATCGAAGATATA 775
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QY 1196 CTACTTTCCCTTTTCTTAAACATATATCTTACAAATTAATCAAAATTTGAAATTTTAAATA 1251
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Qy 1775 AAGCACTCAACACACTTTT-----CTGTACAAATTAATAATTAATAATACCG 1826
Db 1836 TATTACCGAAGCTACATTTTAAAGACCTAATAACAATACCAACGGATTTAAATACGA 1895
Qy 1827 AGATTTTGGTATTTCCTCAAGTACAGTAACATTAACCTTTTAAATCGAAACATACC 1886
Db 1896 GGAGTTTAATATAAGAATATAATCAATATTACATGCTGCACCCCAATACAAAT 1955
Qy 1887 ATT-----TATATTTAATCGTCAGATGATCAAAATCAATTTTAAATCAATGATAA 1937
Db 1956 AGTAACCTATAGCTATCAACAACTAAATGCTTTTCCAAATGATCAATTAATTTATGATAG 2015
Qy 1938 AATTGAATTTATACCAATTAATCTCTCTGTACGCCAAATAGAGAAACAAAATTAGA 1997
Db 2016 AATCGAATTTTATCCAAATGATCAAGGTGTAGTACCTTGTACAGTAAACTTAAAGATTAGA 2075
Qy 1998 AACTATCCAAACAAAATAATACATTTTTCACAAATCATACAAA 2043
Db 2076 AATAACAAAAGAGTTAATTAATCTATTTATTTAGTTAAACAAA 2121

RESULT 15
AF132928
LOCUS
DEFINITION
Bacillus thuringiensis subsp. finitimus Cry28Aa1 delta-endotoxin
gene, complete cds.
ACCESSION
VERSION
AF132928.1 GI:4574729
KEYWORDS
SOURCE
ORGANISM
Bacillus thuringiensis serovar finitimus
Bacillus thuringiensis serovar finitimus
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
REFERENCE
1 (bases 1 to 4896)
Wojciechowska, J.A., Lewitin, E., Revina, L.P., Zalunin, I.A. and
Chestrukina, G.G.
Two novel delta-endotoxin gene families cry26 and cry28 from
Bacillus thuringiensis ssp. finitimus
FEBS Lett. 453 (1-2), 46-48 (1999)
10403372
REFERENCE
2 (bases 1 to 4896)
Wojciechowska, J.A., Lewitin, E.I. and Chestrukina, G.G.
Direct Submission.,
Submitted (04-MAR-1999) Laboratory of Protein Chemistry, Institute
of Microbial Genetics, Dorozhny proezd, Moscow 113545, Russia
Location/Qualifiers
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ORIGIN

Query Match 7.7%; Score 161.2; DB 1; Length 4896;
Best Local Similarity 57.0%; Pred. No. 9.3e-13;
Matches 385; Conservative 0; Mismatches 243; Indels 48; Gaps 3;
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Db 1293 AGGTGGGTACTTATATCAATTTGGAACTTGGCTCCGTTCTTTGGCCTGATCCAGGA 1352
Qy 213 AGA---CAAAACAGTATGGACACAAATTTATATAATGGAGAAATTTTGTGATACAC 269
Db 1353 AGATCCAAAAAATTTGGTCACAAATTTATGAACACGGAGAGACCTTTTAAATCAAA 1412
Qy 270 GTTAACAGAAACATATAAACAGCTAAAGTTACAACTTTTAGAGGATTTAGACAAATAT 329
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Qy 330 ACAAAGCTATAATACAGCATTAGAGATTGGAGAAATTTAAAAAGACTACAAGCTCCTGG 389
Db 1473 ACGTACTATGAAGAGCATTTAATGATTGGAGAGAAATCCAGTGCAATACTGCCAG 1532
Qy 390 ATTACCAACCATCATCAGCATTACAAAGCTGCTTGACTCTTTAAATACGATTGAGAA 449
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Qy 510 ATTACTACTCTATTATGCGCAAGCTGCTAAATTTTTCATTTTAAATTTTATTAACAAGGTGC 569
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Db 1848 TGCTTATAACACATATCGTCGAGAAATGACCTTAATTTGTTATTGGATCTTTGTCGCAACTTT 1907
Qy 810 TTCTTTTATGATATA 825
Db 1908 TCCTTTTATGATATA 1923

Search completed: February 15, 2006, 03:24:50
Job time : 10541 secs

Result No.	Query			ID	Description
	Score	Match	Length		
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2	2085	100.0	2235	13	ADR89396
3	1794.4	86.1	2208	13	ADR89394
4	334.6	16.0	3940	1	AAW93054
5	334.6	16.0	4571	1	AAW93059
6	334.6	16.0	4934	1	AAW81490
7	331.4	15.9	3543	2	AAQ14669
8	331.4	15.9	3543	2	AAQ81178
9	161.2	7.7	4896	6	AAQ43974
10	161.2	7.7	4896	10	ADF31301
11	161.2	7.7	4896	10	ADF31306
12	158	7.6	2061	2	AAQ14670
13	158	7.6	2061	2	AAQ81180
14	148.2	7.1	3756	1	AAW50525
15	117	5.6	15548	6	ABL34155
16	101.2	4.9	3684	1	AAK2106
17	101	4.8	3684	6	ABK14949
18	100.6	4.8	3535	1	AAW91003
19	100.6	4.8	3684	14	AAE61392

ALIGNMENTS

RESULT 1
ADR89398
IID ADR89398 standard; cDNA; 2085 bp.
XX
XX ADR89398;
XX AC
XX DT
18-NOV-2004 (first entry)
XX
XX
XX
XX

ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide; expression cassette; transformation; transgenic; plant; bacteria; lepidoptera; coleoptera; pest; pesticide; resistance; pesticial activity.

Bacillus thuringiensis.	
Key	Location/Qualifiers
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WC2004074462-A2.	

(ATHE-) ATHENIX CORP.

XX Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
XX WPI; 2004-635574/61.
DR P-PSDB; ADR89399.
XX
PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
PS Claim 1; SEQ ID NO 10; 178pp; English.
XX
CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
SQ Sequence 2085 BP; 794 A; 338 C; 302 G; 651 T; 0 U; 0 Other;
Query Match 100.0%; Score 2085; DB 13; Length 2085;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2085; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTCAGGGAATACAAATATGTGTATATTCGAGACATTTGCTAGTGTGTATACA 60
DB 1 ATGTGTCAGGGAATACAAATATGTGTATATTCGAGACATTTGCTAGTGTGTATACA 60
QY 61 ATTGTGTCAGTGTAGTGCAGGTACTATTGTATCCGGTACTCTGTTCGCCGTATAGTGGG 120
DB 61 ATTGTGTCAGTGTAGTGCAGGTACTATTGTATCCGGTACTCTGTTCGCCGTATAGTGGG 120
QY 121 CTCACCTTCATATCCGACCGATAGAAATATAGGTGCTATATATATCTTTTGGTACC 180
DB 121 CTCACCTTCATATCCGACCGATAGAAATATAGGTGCTATATATATCTTTTGGTACC 180
QY 181 CTAATCAGTGTCTTTTGGCCCGGAGAACCAAGACAAACAGTATGGACAAATTTATT 240
DB 181 CTAATCAGTGTCTTTTGGCCCGGAGAACCAAGACAAACAGTATGGACAAATTTATT 240
QY 241 AAAATGGGAGAAATTTTGTGTATACACCGTTAAACAGAAAGCATAAAACAGCTAAAGTTA 300
DB 241 AAAATGGGAGAAATTTTGTGTATACACCGTTAAACAGAAAGCATAAAACAGCTAAAGTTA 300
QY 301 CAAACTTTAGAGGATTTAGACAAATATTACAAAGCTATAATACAGCATTAGATGTTGG 360
DB 301 CAAACTTTAGAGGATTTAGACAAATATTACAAAGCTATAATACAGCATTAGATGTTGG 360
QY 361 AGAAATTTAAAGACTACAGCTCTCGATTTACCAACCATCATCAGCATTTACAAAGCT 420
DB 361 AGAAATTTAAAGACTACAGCTCTCGATTTACCAACCATCATCAGCATTTACAAAGCT 420
QY 421 GCCTTGACTCTTAAATACGATTTGAGATGTTTACAATGATTTTATTCGAGAAATACCT 480
DB 421 GCCTTGACTCTTAAATACGATTTGAGATGTTTACAATGATTTTATTCGAGAAATACCT 480
QY 481 GGTTCCTCACTTGAACCTTATAAAGCCTATTACTACCTATTATCGGCAAGCTGCTAAT 540
DB 481 GGTTCCTCACTTGAACCTTATAAAGCCTATTACTACCTATTATTCGCAAGCTGCTAAT 540
QY 541 TTTTCATTTAAATTTATTACAAAGGTGCTGAATTTGGCTGATGAATGGAATGCAGATATA 600
DB 541 TTTTCATTTAAATTTATTACAAAGGTGCTGAATTTGGCTGATGAATGGAATGCAGATATA 600

QY 601 CATCTTTCACAAATTTGAACCTAATGCTGGAAACATCAGATGACTATTATATAAATCTTTTAAAA 660
DB 601 CATCTTTCACAAATTTGAACCTAATGCTGGAAACATCAGATGACTATTATATAAATCTTTTAAAA 660
QY 661 GAAAAATATACCTTAAATATAGTAACTATTGTGCAAAATCCTATAGAGAAGGACTTAAATAA 720
DB 661 GAAAAATATACCTTAAATATAGTAACTATTGTGCAAAATCCTATAGAGAAGGACTTAAATAA 720
QY 721 CTTTCAAAAGCAACCTTAAATATAGATGGAGTATATTAAATGATTTATCGAGATATATGACT 780
DB 721 CTTTCAAAAGCAACCTTAAATATAGATGGAGTATATTAAATGATTTATCGAAGATATATGACT 780
QY 781 ATTACTGTATTAGATACCTATCGCTCAATTTCTTTTATGATATAAAGAGATACAAAGAT 840
DB 781 ATTACTGTATTAGATACCTATCGCTCAATTTCTTTTATGATATAAAGAGATACAAAGAT 840
QY 841 TCAATAGGAAGAATAGGTGGCAATTAAAACTGAACTTCAAGAGAAATTTATACAACCTGAA 900
DB 841 TCAATAGGAAGAATAGGTGGCAATTAAAACTGAACTTCAAGAGAAATTTATACAACCTGAA 900
QY 901 ATAAATTTTGACCGCTTACTTACCTTGAATTTCAACCCAACTCGCTATATGGAATAT 960
DB 901 ATAAATTTTGACCGCTTACTTACCTTGAATTTCAACCCAACTCGCTATATGGAATAT 960
QY 961 AATTTTAAACAGTTCAGGCGCTTAGATTTATTTTCAATTTTAGATGAACTTATATTTATACA 1020
DB 961 AATTTTAAACAGTTCAGGCGCTTAGATTTATTTTCAATTTTAGATGAACTTATATTTATACA 1020
QY 1021 AAAAAATGAAACGTACGGGAATCGTTTAGTGTGATTTGCGAATTCGTAATAGATCTACTTAT 1080
DB 1021 AAAAAATGAAACGTACGGGAATCGTTTAGTGTGATTTGCGAATTCGTAATAGATCTACTTAT 1080
QY 1081 GCTACGACAGGAATCTGAAATTTATATATGAGAGAAAGACAGGTCACCCCAACAAAAACT 1140
DB 1081 GCTACGACAGGAATCTGAAATTTATATATGAGAGAAAGACAGGTCACCCCAACAAAAACT 1140
QY 1141 TTAATACCAATTTGGAATCCTATAAAGTTTCAATTTGTAACCTGATAGACAAGTAACTCTACT 1200
DB 1141 TTAATACCAATTTGGAATCCTATAAAGTTTCAATTTGTAACCTGATAGACAAGTAACTCTACT 1200
QY 1201 TCCCTCTTTTCTTAAACATATACCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 1260
DB 1201 TCCCTCTTTTCTTAAACATATACCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 1260
QY 1261 CCTAGTAAATAAATAAATAATTAATTAATACAGTGGGGGAAATTTATCTAAATGATTAATAAACA 1320
DB 1261 CCTAGTAAATAAATAAATAATTAATTAATACAGTGGGGGAAATTTATCTAAATGATTAATAAACA 1320
QY 1321 GATTTTCAATTTCTGTAAAAAAGACTGTAACCAATTTATTAATCCAAATTTGTTTACCA 1380
DB 1321 GATTTTCAATTTCTGTAAAAAAGACTGTAACCAATTTATTAATCCAAATTTGTTTACCA 1380
QY 1381 AGCTATAATAGTATTAGTCATATTTTATCCCAAGTTTCTTTTATTTAAATTTTCTTATAA 1440
DB 1381 AGCTATAATAGTATTAGTCATATTTTATCCCAAGTTTCTTTTATTTAAATTTTCTTATAA 1440
QY 1441 ATTGGAATAGCGCTTAAATATATTAATTAATACAGTGGGCAATTTAGGATGGACACACAGTAGTGT 1500
DB 1441 ATTGGAATAGCGCTTAAATATATTAATTAATACAGTGGGCAATTTAGGATGGACACACAGTAGTGT 1500
QY 1501 AATAGAAATATGCAATATCAGATAAAATTAATTAATGATCCCAAGCAATCAAGAGTAAC 1560
DB 1501 AATAGAAATATGCAATATCAGATAAAATTAATTAATGATCCCAAGCAATCAAGAGTAAC 1560
QY 1561 AGTCTTTGATACAAACTCTAAAGGTAAATGGAAGGACCTGGTCTATACAGGAGGAACTTGGTT 1620
DB 1561 AGTCTTTGATACAAACTCTAAAGGTAAATGGAAGGACCTGGTCTATACAGGAGGAACTTGGTT 1620
QY 1621 TATTTTCAAAAGTCAAGGCGTTTAGAGATTACATGTAGAACTCTCTAAATTTCTTACAAATCT 1680
DB 1621 TATTTTCAAAAGTCAAGGCGTTTAGAGATTACATGTAGAACTCTCTAAATTTCTTACAAATCT 1680
QY 1681 TATTACATTAGACTTCGATACGCTACAAATGGTGTGGAAATACTCTTCTCTTAATATATCT 1740

1681 TATTACATTAGACTTCGATACGCTACAAATGGGCTGGAAATACTCTTCTTAATATATCT 1740
1741 CTTTACAAATACAGGAGTAATAGGAATACCACTCAACGACTCAACACACTTTTCTGGT 1800
1741 CTTTACAAATACAGGAGTAATAGGAATACCACTCAACGACTCAACACACTTTTCTGGT 1800
1801 ACAAATTAATTAATTTACAAATACGAGATTTGGGTATTTCCAAATTTCCAAATGTA 1860
1801 ACAAATTAATTAATTTACAAATACGAGATTTGGGTATTTCCAAATTTCCAAATGTA 1860
1861 ACATTTACCTTTAAATCGAAATACCACTTTATTTAATCGTGAGATGATCAAAATCA 1920
1861 ACATTTACCTTTAAATCGAAATACCACTTTATTTAATCGTGAGATGATCAAAATCA 1920
1921 ATTTTATCATTTGATAAAATTTGAATTTATACCAATTTACTTCTCTGTACGCCAAATAGA 1980
1921 ATTTTATCATTTGATAAAATTTGAATTTATACCAATTTACTTCTCTGTACGCCAAATAGA 1980
1981 GAAAAACAAAATTTAGAACTATCCAAACAAAATTAATATATTTTTCACAAATCATACA 2040
1981 GAAAAACAAAATTTAGAACTATCCAAACAAAATTAATATATTTTTCACAAATCATACA 2040
2041 AAAAAATCTTTAATATAGAGCCACAACTATGATATTGATTA 2085
2041 AAAAAATCTTTAATATAGAGCCACAACTATGATATTGATTA 2085

RESULT 2
ADNR89396
ID ADNR89396 standard; cDNA; 2235 BP.
XX AC
XX AC
XX ADNR89396;
DT 18-NOV-2004 (first entry)
XX
XX AXMI-007 coding sequence.
KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
XX Bacillus thuringiensis.
XX Key Location/Qualifiers
XX CDS 1..2235
XX FT /tag= a
XX FT /product= "AXMI-007"
XX FT /transl_except= pos:1..3, aa:Met
XX
XX WO2004074462-A2.
XX
XX PD 02-SEP-2004.
XX
XX 20-FEB-2004; 2004WO-US005829.
XX
XX 20-FEB-2003; 2003US-0448632P.
XX 20-FEB-2003; 2003US-0448633P.
XX 20-FEB-2003; 2003US-0448797P.
XX 20-FEB-2003; 2003US-0448806P.
XX 20-FEB-2003; 2003US-0448810P.
XX 20-FEB-2003; 2003US-0448812P.
XX 19-FEB-2004; 2004US-00781979.
XX 19-FEB-2004; 2004US-00782020.
XX 19-FEB-2004; 2004US-00782096.
XX 19-FEB-2004; 2004US-00782141.
XX 19-FEB-2004; 2004US-00782570.
XX 19-FEB-2004; 2004US-00783417.
XX
XX (ATHE-) ATHENIX CORP.
XX Carozzi N, Hargiss T, Kozziel MG, Duck NB, Carr B;
PI

XX WPI: 2004-635574/61.
DR P-PSDB; ADR89397.
XX
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
XX Claim 1; SEQ ID NO 8; 178pp; English.
XX
XX This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
XX Sequence 2235 BP; 861 A; 364 C; 316 G; 694 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 2085; DB 13; Length 2235;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2085; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTGTCAGGGAATACAAATATGGTGATAATTTTCGAGACATTTGCTAGTGTGATACA 60
Db 151 ATGTGTCAGGGAATACAAATATGGTGATAATTTTCGAGACATTTGCTAGTGTGATACA 210
Qy 61 ATTGTCAGTGTAGTGCAGGTACTATTGTATCCGGTACTCTGTAGCCGGTATAGTGGG 120
Db 211 ATTGTCAGTGTAGTGCAGGTACTATTGTATCCGGTACTCTGTAGCCGGTATAGTGGG 270
Qy 121 CTGACTTCTATATCCGACCGATAGGAATTAAGTGTCTATTAATAATATCTTTTGGTACC 180
Db 271 CTCACCTTCTATATCCGACCGATAGGAATTAAGTGTCTATTAATAATATCTTTTGGTACC 330
Qy 181 CTAATCACTGTCTTTTCGCCGGGAGAACAAACAAACAGTATGACACAAATTTATT 240
Db 331 CTAATCACTGTCTTTTCGCCGGGAGAACAAACAAACAGTATGACACAAATTTATT 390
Qy 241 AAAATGGGAGAAATTTTGTGTATACACCGTTAAACAGAAAGCATAAAACAGCTAAAGTTA 300
Db 391 AAAATGGGAGAAATTTTGTGTATACACCGTTAAACAGAAAGCATAAAACAGCTAAAGTTA 450
Qy 301 CAAACTTTAGAGGATTTAGACAAATATTACAAAGCTATATACAGCATTTAGATGATTGG 360
Db 451 CAAACTTTAGAGGATTTAGACAAATATTACAAAGCTATATACAGCATTTAGATGATTGG 510
Qy 361 AGAAATTTAAAGACTACAGCTCCCTGGATTACACCATCATCAGCATTTACAAAGCT 420
Db 511 AGAAATTTAAAGACTACAGCTCCCTGGATTACACCATCATCAGCATTTACAAAGCT 570
Qy 421 GCCTTTGACTCTTAAAAATACGATTTGAGAAATGTTTCAATGATTTTATTCGAGAAATACCT 480
Db 571 GCCTTTGACTCTTAAAAATACGATTTGAGAAATGTTTCAATGATTTTATTCGAGAAATACCT 630
Qy 481 GGTTCCTCAACTTTGAAACTTTATAAAACCGTATTACTACCTATTATTCGCCAAGCTGCTAAT 540
Db 631 GGTTCCTCAACTTTGAAACTTTATAAAACCGTATTACTACCTATTATTCGCCAAGCTGCTAAT 690
Qy 541 TTTTCATTTAAATTTATTAACAAAGGCTCGTAATGGCTGATGAATGAATGCAGATATA 600
Db 691 TTTTCATTTAAATTTATTAACAAAGGCTCGTAATGGCTGATGAATGAATGCAGATATA 750
Qy 601 CATCCTTCACAAATTTGAACCTTAATGCTGGAACATCAGATGATATATAAATTTTAAAA 660

Db 751 CATCTTTCACAAATTGAACTTAATGCTGGAAACATCAGATGACTATTATATAAACTTTTAAAA 810
Qy 661 GAAATATATACCTAAATATATAGTAATCTATGTGCAAAATACCTATAGAGAAGGACTTAAATAAA 720
Db 811 GAAATATATACCTAAATATATAGTAATCTATGTGCAAAATACCTATAGAGAAGGACTTAAATAAA 870
Qy 721 CTTTGAAGCAACCTAATATGAGATGGAGTATATTTTAATGATATATCGAAGATATATGACT 780
Db 871 CTTTGAAGCAACCTAATATGAGATGGAGTATATTTTAATGATATATCGAAGATATATGACT 930
Qy 781 ATTACTGTATATAGATACTATCGCTCAATTTCTTTTATGATATAAGAGATACAAAGAT 840
Db 931 ATTACTGTATATAGATACTATCGCTCAATTTCTTTTATGATATAAGAGATACAAAGAT 990
Qy 841 TCAATAGGAAGATAGGTGGCAATTAAGAACTGAACTTCAAGAGAAATTTATACAACCTGAA 900
Db 991 TCAATAGGAAGATAGGTGGCAATTAAGAACTGAACTTCAAGAGAAATTTATACAACCTGAA 1050
Qy 901 ATAAATTTTGACGCTCTTACTTACCTTGAAATTCAAACCAATCTCGCTATATATGGAATAT 960
Db 1051 ATAAATTTTGACGCTCTTACTTACCTTGAAATTCAAACCAATCTCGCTATATATGGAATAT 1110
Qy 961 AATTTAACAAGCTTACAGGCTTATGATATTTTCAATTTTATAGATGAACCTTATATTTATACA 1020
Db 1111 AATTTAACAAGCTTACAGGCTTATGATATTTTCAATTTTATAGATGAACCTTATATTTATACA 1170
Qy 1021 AAAAAATGAACCTGACGGGAATCGTTAGTTGGTATTCGAAATCGTAAATAGATCTACTTAT 1080
Db 1171 AAAAAATGAACCTGACGGGAATCGTTAGTTGGTATTCGAAATCGTAAATAGATCTACTTAT 1230
Qy 1081 GCTACGACAGGAACCTGAATTTATATGAGAAAGAACAGGTCACCCACACAAACAACT 1140
Db 1231 GCTACGACAGGAACCTGAATTTATATGAGAAAGAACAGGTCACCCACACAAACAACT 1290
Qy 1141 TTAATACCAATTTGAATCCTATAAAGTTTCAATTTGTAATGATAGACAAAGTAACTCTACT 1200
Db 1291 TTAATACCAATTTGAATCCTATAAAGTTTCAATTTGTAATGATAGACAAAGTAACTCTACT 1350
Qy 1201 TCCCTTTTCTTAACATATACCTTACAAATTAATCAAAATTTGAATTTAATTAATTAATCA 1260
Db 1351 TCCCTTTTCTTAACATATACCTTACAAATTAATCAAAATTTGAATTTAATTAATTAATCA 1410
Qy 1261 CCTAGTAATATAATTAACATATTCAGCTGGGGGAATTTATCTAATGATATAAAACAACT 1320
Db 1411 CCTAGTAATATAATTAACATATTCAGCTGGGGGAATTTATCTAATGATATAAAACAACT 1470
Qy 1321 GATTTTCAATTTCTCTAATAAAGACTGTAAACCAATTTAATTAATCCTAATTTGTTTACCA 1380
Db 1471 GATTTTCAATTTCTCTAATAAAGACTGTAAACCAATTTAATTAATCCTAATTTGTTTACCA 1530
Qy 1381 AGCTATAATAGTTATAGTCAATTTTATCCAGTTTCTTTTATTTAATTTATTTCTCTATAAA 1440
Db 1531 AGCTATAATAGTTATAGTCAATTTTATCCAGTTTCTTTTATTTAATTTATTTCTCTATAAA 1590
Qy 1441 ATTGGATTAGCGCTAATATATATATATACAGTGGCAATTTAGGATGGACACACAGTAGTGT 1500
Db 1591 ATTGGATTAGCGCTAATATATATATATACAGTGGCAATTTAGGATGGACACACAGTAGTGT 1650
Qy 1501 AATAGAAATAATGCAATATCAGATAAAATAATTAACAATGATCCAGCAATCAAGAGTAACT 1560
Db 1651 AATAGAAATAATGCAATATCAGATAAAATAATTAACAATGATCCAGCAATCAAGAGTAACT 1710
Qy 1561 AGTCTTTGATACAAACTCTAAGGTAATTTGAAGGACCTGGTCATACAGGAGGAACTTGGTT 1620
Db 1711 AGTCTTTGATACAAACTCTAAGGTAATTTGAAGGACCTGGTCATACAGGAGGAACTTGGTT 1770
Qy 1621 TATTTACAAGCTCAAGGGGTTTAGAGATTAATGATAGAACTCTTAATTTCTACAACTCT 1680
Db 1771 TATTTACAAGCTCAAGGGGTTTAGAGATTAATGATAGAACTCTTAATTTCTACAACTCT 1830
Qy 1681 TATTACATTTAGACTTCGATACGCTACAAATGGTGGTGGAAATACTCTTCTAATATATCT 1740
Db 1831 TATTACATTTAGACTTCGATACGCTACAAATGGTGGTGGAAATACTCTTCTAATATATCT 1890

Qy 1741 CTTTCAATACACAGGAGTAAATAGGAATACCACTCAACGACTCAACAACTTTTCTGGT 1800
Db 1891 CTTTCAATACACAGGAGTAAATAGGAATACCACTCAACGACTCAACAACTTTTCTGGT 1950
Qy 1801 ACAAAATTAATAAATTTTACAATACGAGATTTTGGGTATTTCCAAATTTTCCAAAGTACAGTA 1860
Db 1951 ACAAAATTAATAAATTTTACAATACGAGATTTTGGGTATTTCCAAATTTTCCAAAGTACAGTA 2010
Qy 1861 ACATTACCTTTTAAATCGAAACATACCATTTATTTAATCGTGCAGATGTATCAAAATTC 1920
Db 2011 ACATTACCTTTTAAATCGAAACATACCATTTATTTAATCGTGCAGATGTATCAAAATTC 2070
Qy 1921 ATTTTAATCATTTGATATAAATTTGAATTTATACCAATTTACTTCTGTACGCCAAATATAG 1980
Db 2071 ATTTTAATCATTTGATATAAATTTGAATTTATACCAATTTACTTCTGTACGCCAAATATAG 2130
Qy 1981 GAAAAACAAAATTTAGAACTATCCAAACAAAATAAATACATTTTTCACAAATCATACA 2040
Db 2131 GAAAAACAAAATTTAGAACTATCCAAACAAAATAAATACATTTTTCACAAATCATACA 2190
Qy 2041 AAAAAATACCTTTTAAATATAGAACCCAAACTATGATATTTGATTAA 2085
Db 2191 AAAAAATACCTTTTAAATATAGAACCCAAACTATGATATTTGATTAA 2235
RESULT 3
ADR89394
ID ADR89394 standard; cDNA; 2208 BP.
XX ADR89394;
AC ADR89394;
XX DT 18-NOV-2004 (first entry)
XX AXMI-006 coding sequence.
XX ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
OS Bacillus thuringiensis.
XX Key Location/Qualifiers
FH 1. :2208
FT /*tag= a
FT /product= "AXMI-006"
XX WO2004074462-A2.
PD 02-SEP-2004.
XX 20-FEB-2004; 2004WO-US005829.
XX 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX (ATHE-) ATHENIX CORP.
PA Carozzi N, Hargiss T, Kozziel MG, Duck NB, Carr B;
XX WPI; 2004-635574/61.
DR P-PSDB; ADR89395.

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
PS Claim 1; SEQ ID NO 6; 178pp; English.
XX
CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
SQ Sequence 2208 BP; 842 A; 377 C; 308 G; 681 T; 0 U; 0 Other;
Query Match 86.1%; Score 1794.4; DB 13; Length 2208;
Best Local Similarity 92.7%; Pred. No. 3.9e-290;
Matches 1908; Conservative 0; Mismatches 141; Indels 9; Gaps 2;
1 ATGTGTCAGGGAATACACAATATGGTGATAATTTTCAGACATTTGCTAGTGTGATACA 60
154 ATGTGTCAGGGAATACACAATATGGTGATAATTTTCAGACATTTGCTAGTGTGATACA 213
61 ATGTGTCAGTGTAGTCAGGTACTATTGTATCCGGTACTCTGTAGCCGGTATAGTGGG 120
214 ATGTGTCAGTGTAGTCAGGTACTATTGTATCCGGTACTCTGTAGCCGGTATAGTGGG 273
121 CTGACTTCTATATCCGACCGATAGGAATATAGGTGCTATAATATCTTTTGGTACC 180
274 CTCACCTTCTATATCCGACCGATAGGAATATAGGTGCTATAATATCTTTTGGTACC 333
181 CTATCACTGTCTTTTGGCCGCGGGAACAACAGACAAAACAGTATGGACACAAATTTATT 240
334 CTATCACTGTCTTTTGGCCGCGGGAACAACAGACAAAACAGTATGGACACAAATTTATT 393
241 AAAATGGGAGAAATTTTGTGTATACACCGTTAAACAGAAAGCATAAAACAGCTTAAAGTTA 300
394 AAAATGGGAGAAATTTTGTGTATACACCGTTAAACAGAAAGCATAAAACAGCTTAAAGTTA 453
301 CAAACTTTAGAGGATTTAGACAAATATTACAAAGCTATATACAGCATTAGATGATTGG 360
454 CAAACTTTAGAGGATTTAGACAAATATTACAAAGCTATATACAGCATTAGATGATTGG 513
361 AGAAAAATTAAGACGTACAGCTCTCGGATTACACCATCATCAGCATTTACAAACAAGCT 420
514 AGAAAAATTAAGACGTACAGCTCTCGGATTACACCATCATCAGCATTTACAAACAAGCT 573
421 GCCTTGACTCTTAAATAACGATTTGAGAAATGTTTCAATAGATTTTATTCGAGAAATACCT 480
574 GCCTTGACTCTTAAATAACGATTTGAGAAATGTTTCAATAGATTTTATTCGAGAAATACCT 633
481 GGTTCGAACTTGAACTTATAAAGCTATTACTCTATTATTCGCAAGCTGCTTAAT 540
634 GGTTCGAACTTGAACTTATAAAGCTATTACTCTATTATTCGCAAGCTGCTTAAT 693
541 TTTTCATTTAAATTTATTACAAACAGGCTGCTGAATGGCTGATGAATGGAATGCAGATATA 600
694 TTTTCATTTAAATTTATTACAAACAGGCTGCTGAATGGCTGATGAATGGAATGCAGATATA 753
601 CATCTTTCACAAATTTGAACCTTAATGCTGGAAACATCAGATGACTATTATTAATTTTAAAA 660
754 CATCTTTCACAAATTTGAACCTTAATGCTGGAAACATCAGATGACTATTATTAATTTTAAAA 813
661 GAAATATACCTTAATATAGTAACTATTGTGCAATACCTATAGAGAAGGACTAAATATA 720

814 GAAATATACCTTAATATAGTAACTATTGTGCAAAATACCTATAGAACAGGACTAAAAAT 873
721 CTTGCAACAGCACTTAATATAGATGGAGTATTTAATGATTATTCGAAGATATATGACT 780
874 CTTAGAGACGAACCAAAATATGAATGGAGTATTTAATGACTATTCGAAGATATATGACC 933
781 ATTACTGTATTAGATACTATCGCTCAATTTTCTTTTATGATATAAAGAGATACAAAGAT 840
934 ATTACTGTATTAGATACCACTCTCAATTTTCTTTATATGATATAAAGAGATATAGAGAT 993
841 TCAATAGGAGGAATAG-----GTGGCATTAACCTGAACTTACAAGAGAAATTTATACA 894
994 TCAATAGGAGGAATAGAAAGGCAATTAAGAATGAACCTCAAGAGAAATTTATACA 1053
895 ACTGAATTAATTTTGAACCGCTCTTACTTACCTTTGAAATTTCAACCCCAATCTCGCTATAATG 954
1054 ACTGAATTAATTTTGTGCTCTTCTCAACTTAGAGTTTCAACCCCAATCTAGCTACGATG 1113
955 GAATATAATTTAACACGTTTCAAGGCTTAGATTAATTTTCAATTTTATAGATGAACCTTATTT 1014
1114 GAATATAATTTAACACGTTTCAAGGCTTAGATTAATTTTCAATTTTATAGATGAACCTTATTT 1173
1015 TATACAAAAATGAACGTAACGTAACGTTAGTTGGTATTCGGAATCGTAAATAGATCT 1074
1174 TATACAGAAAAATACAAATTTTCGGAATCGTTAGTTGGTATTTCTAATCGTGTACACCT 1233
1075 ACTTATGCTACGACAGGAAGTGAATATATATATGGAGAAAGACAGCTCCACCCACAACA 1134
1234 ACTTATAGCAATACTATACTGAACCTTTATATGGAGAAAGAACAGGTTCCACCCACAACA 1293
1135 AAAACCTTTAATACATTTGAATCCTATAAAGTTTCAATTTGTAACCTGATAGACAACTAAT 1194
1294 AAAACCAATTAAGCACTTTGNACTTATAAAGTTTCAATTTGTAACCTGATAGACAACTAAT 1353
1195 CCTACTTCCCTTTTCTTAACATATCTTTCAATTAATCAAATTTGAACCTTTATTTAAAT 1254
1354 CCTGTTTCCCTATTC---AACCACTTTTATAAATTAATCAAATTTGAACCTTTATTTAAAT 1410
1255 AATTCACCTAGTAAATAATTAACATATTCAGCTGGGGGAATTTATCTAATGATATAAAAA 1314
1411 GGCTCATATAACAAACACCTCAAAATTTTCAGAGAGAGGGTCTTTATCTAATATCAAAAC 1470
1315 ACAACTGATTTTCAATTTCTGTAAAAAAGACAGCTGTAACCAATTTAATTTCAAAATTTGT 1374
1471 ACACTTTTCTCAATTTCTTAGAAAAAGACAGCTGCAATCTAGTTATTGATCCAGGTTGT 1530
1375 TTACCAAGCTATTAATAGTTATAGTCAATTTTATCCAGTTTCTTTTATTTTATTTATTC 1434
1531 TCACCAAACTTTAATAACTATAGTCAATTTTATCCCATTTTTCATTTATTTTATTTTC 1590
1435 TATATAATTTGATTTAGCGCTTAATATATATATACAGGTGCATTTAGGATGGACACAGT 1494
1591 TATGTGATTTGGATTTACAGCTCAAAATTTAGATACAGGTGATTTAGGATGGACACAGT 1650
1495 AGTGTTAATAAGAAATTAATGCAATATCAGATAAAATAATTAACAATGATCCAGCAATCAA 1554
1651 AGTGTGATAGATATATGCAATATCAGATAAAATAATTAACAATGATCCAGCAATCAA 1710
1555 GGTAACAGCTCTTGATACAAACTCTTAAGGTAATTTGAAGGACCTGTGTCATACAGGAGGAAC 1614
1711 GGTAACCAATCTTGATACAAACTCTTAAGGTAATTTGAAGGACCTGTGTCATACAGGAGGAAC 1770
1615 TTGGTTTATTTACAAAGCTCAAGGCGTTTGAAGATTACATGTAGAACTCTCTTAATTTCTACA 1674
1771 TTGGTTTATTTACAAAGCTCAAGGCGTTTGAAGATTACATGTAGAACTCTCTTAATTTCTACA 1830
1675 CAATCTTATTTACATTTAGACTTTCGATACCAATTTGCTGCGAAATFACCTTTCTCTAAT 1734
1831 CAATCTTATTTTCAATTTAGACTTTCGATACCAATTTGCTGCGAAATFACCTTTCTCTAAT 1890
1735 ATATCTCTTCAATATACAGGAGTAAATAGGAATACCACTCAACGACTCAACACACTTTT 1794

Db 1891 ATATCTCTTACAATACAGGAGTAATAGGAATACCACCTCAACGACTCAACAAACACTTTT 1950
QY TCTGGTACAAATTAATAATTTACAATACGGAGATTTTGGGTATTTTCCAATTTCCAAGT 1854
Db 1951 TCTGGTACAAATTAATAATTTACAATACGGAGATTTTGGGTATTTTCCAATTTCCAAGT 2010
QY 1855 ACAGTAACATTTACCTTTAAATCGAAACATACGATTTATATTTAATCGTGCAGATGTATCA 1914
Db 2011 ACAGTAACATTTACCTTTAAATCGAAACATACGATTTATATTTAATCGTGCAGATGTATCA 2070
QY 1915 AATTCATTTTAAATCATGTAATTAATTTGAATTTTATACCAATTTCTCTGTACGCCAA 1974
Db 2071 AATTCATTTTAAATCATGTAATTAATTTGAATTTTATACCAATTTCTCTGTACGCCAA 2130
QY 1975 AATAGAGAAAAACAAAAATTTAGAACTATCCAAACAAAAAATAAATACATTTTTCACAAAT 2034
Db 2131 AATAGAGAAAAACAAAAATTTAGAACTATCCAAACAAAAAATAAATACATTTTTCACAAAT 2190
QY 2035 CATACAAAAAATCTTTA 2052
Db 2191 CATACAAAAAATCTTTGA 2208

RESULT 4

AAN93054
ID AAN93054 standard; DNA; 3940 BP.

XX
AC AAN93054;

DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)

DT 30-MAY-1990 (first entry)
XX

DE Delta-endotoxin crystal protein gene.
XX

XX Delta-endotoxin; crystal protein; insecticide; ss; pCC130;
KW biological control agent.

XX Bacillus thuringiensis; israelensis.
OS

EH Key Location/Qualifiers
FT RBS 879. .884

FT /*tag= b
FT /*label= Shine-Delgarno sequence

FT CDS 891
FT /*tag= a

FT /*product= "delta-endotoxin"
XX

PN EP296870-A.
XX

PD 28-DEC-1988.
XX

XX 24-JUN-1988; 88EP-00305772.
PF

XX 26-JUN-1987; 87US-00067653.
PR

XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX

XX Ellar DJ, Ward ES;
XX

XX WPI; 1989-001322/01.
XX

DR P-PSDB; AAP94035.
DR

XX DNA fragment encoding insecticidal protein - obtd. from Bacillus
XX

XX thuringiensis sub species israelensis, and used in microorganisms and
XX

XX plant cells.
XX

XX Disclosure; Fig 5; 26pp; English.
PS

XX The nucleotide sequence is an insert in plasmid pCC130. The delta
XX

CC endotoxin protein is insecticidal and can be used to control insect pests
CC

CC esp. mosquitoes. See also AAN93059. (Updated on 25-MAR-2003 to correct PA
CC

field.) (Updated on 27-AUG-2003 to correct OS field.)
..CC

XX SQ Sequence 3940 BP; 1457 A; 603 C; 659 G; 1221 T; 0 U; 0 Other;
Query Match 16.0%; Score 334.6; DB 1; Length 3940;
Best Local Similarity 53.9%; Pred. No. 1.1e-46;
Matches 858; Conservative 0; Mismatches 695; Indels 38; Gaps 7;
QY 499 TATAAAGCTATTTACTTACCTATTTATGGCGAAGCTGCTAAATTTTCATTTAAATTTATTA 558
Db 1494 TATAACATACTAGTATTATCTAGTTATGCACAAGCAGCAAACTTACATCTGCTGTATTA 1553
QY 559 CAACAAGGTGCTGAATGGCTGATGAATGGAATCGAGATATACATCTTCCACAAAATGAA 618
Db 1554 AATCAAGCGCTCAAAATTTGAAGCGTATTAAAAAACAATCGACAATTCGATTTATTTAGAG 1613
QY 619 CCTAATGCTGGAACTACAGATGACTATTATAAACTTTTAAAAAGAAATATACCTAAATAT 678
Db 1614 CCTTTGCC---AACAGCAATTCGATTTATTCAGTATTCGACTTAAGCTATAGAAGATTAC 1670
QY 679 AGTAACCTATTGTGCAAAATACCTATAGAGAGAGCTAAATAAACTTCGAAACGNAACCTAAT 738
Db 1671 ACTAATTTATTGTGTAAACCACTTATAAAAAAGGATTAAATTTTAAATTTAAAAACGACGCTGAT 1730
QY 739 ATGAGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACT 798
Db 1731 AGTAATCTTTGATGGAAATATAAACTGGAAACATACATACGATATCGAACAAAAATGACT 1790
QY 799 ATCGCTCAATTTTCTTTTATGATATAAAGAGATACAAAGATTTCATATAGGAAGAATAGGT 858
Db 1791 ACTGCTGATTTAGATGTTGTTGCACTCTTTCTTAATATGATGTAGTAAATATCCAAATA 1850
QY 859 GGCATTAAACCTGAACCTTACAAGAGAAATTTATACACTGAAATATAATTTTGACCGTCTTT 918
Db 1851 GGTGTCCAATCTGAACCTTACTCGAGAAATTTAT-----CAGGTACTTTAACTTCGAAGA 1903
QY 919 ACTTACCTTGAATTTCAACCCCAATCTCGCTAATATGGAATATAATTTTACACGTTTCAGGG 978
Db 1904 AAGCCCCCTATAAAATATTATGACTTTTCAATATCAAGAGGATTCCTTTACAGCTAGACCGCA 1963
QY 979 CTTAGATTATTTTCAATTTTATAGTGAACCTTATATTTTATACAAAAAATGAAACGTACGGG 1038
Db 1964 TTTATTACTTGGCTTGATCTTTTGAATTTTATGAAAAAGCGCAAACTACTCTTAATAA 2023
QY 1039 AATCGTTTAGTTGGTATTCGGAATCGTAATAGATCTACTT-ATGCTACACAGGAACTGA 1097
Db 2024 TTTTTCACAGCCATTATAATATGTTTCATTTACACACTTGATAATATATCCCAAAATC 2083
QY 1098 AATTATATATGGAGAAAGAACAGGTCACCCACACAAAAAATTTTAAATACCATTTTGAATC 1157
Db 2084 TAGTGTTTTTGGAAATCAATGTAACGTGATAAAATTTAAATCTCTTGGTTTGGCAACAA 2143
QY 1158 CTATAAAGTTTCAATTTGTAACCTGATAGACAAGTAACTCTACTTCCCTTTTCCCTAACAT 1217
Db 2144 TATTTATATTTTTTTTATTAATGTCATAAGCTTAGATAATAAATATCTAAATGATATATA 2203
QY 1218 ATACTTTTACAATTAATCAAAATTTGAACTTTTATTAATAATTTCCACCTAGTAAATAATTAAC 1277
Db 2204 TAAATATTAGTAAATGCGATTTTTTTTATAACTAATGCTACTAGACTTTTGGGAAAGAACT 2263
QY 1278 ATATTCAGCTGGGGGAATTTTATCTAATGATAAAAAAACAACCTGATTTTCAATTTCTCTGT 1337
Db 2264 TACAGCAGGATCTGGGCAAAATCACTTATGATGATAAATAAATAATTTTCGGGTACCAAT 2323
QY 1338 AAAAAAAGACTGTAAACCAATTTTAAATCCAAATTTGTTTACCAAGCTATAATAGTTATAG 1397
Db 2324 TCTTAAACGAAGAGAGAGAAATCAAGGAAACCTTACCCTTTTCCCAACATATGATAAATATAG 2383
QY 1398 TCATATTTTATCCAGTTTCTTTTATTTAAATTTTCTTATAAATTTGGATTAGCGCTAAA 1457
Db 2384 TCATATTTTATCATTTTATTTAAAGTCTTAGTATCCC-----TGCACACATA 2428
QY 1458 TATATTATATACAGGTGCAATTAGGATGGACACACAGTAGTGTTAATAGAAAATAATGCAAT 1517

Db	2382	AGCCCTTATAAATATATGACCTTCAATATCAAGAGGATTCCTTACACGTAGACCGCA	2441
Qy	979	CTTAGATTATTTTCAATTTTATAGATGAACCTTATATTTATACAAAAAATGAACGTCAGGG	1038
Db	2442	TTTATTTACTTGGCTTGATCTTTGAATTTTATGAAAAAGCGCAACTACTCTTAATAA	2501
Qy	1039	AATCGTTTGTGTTGTTATCGGAATCGTAATAGATCTACTT-ATGCTACACAGGAACTGA	1097
Db	2502	TTTTTTTACCAGCCATTATAATATGTTTCATTACACACTTGATATATATCCCAAAAAATC	2561
Qy	1098	AATTATATATGAGAAAGACAGGTCCACCACCAACAAAACTTTAATACCATTTGAATC	1157
Db	2562	TAGTGTGTTTGGAAATACAAATGTAACATGATTAATTTAAATCTCTTGGTTGGCAACAA	2621
Qy	1158	CTATAAGTTTCAATTTGTAACCTGATAGACAAGTAACCTCTACTTCCCTTTTCCCTAACAT	1217
Db	2622	TATTTATATTTTATTAATGCTCATAGCTTAGATAATAATATCTAAATGATTATAA	2681
Qy	1218	ATACTTTACAAATTAATCAAAATGAACTTTATTTAAATTAATTCACCTAGTAATAAATTAAC	1277
Db	2682	TAATATTAGTAAATGGAATTTTATTAATACTAATGTTACTAGACTTTTGGAGAAAGAAT	2741
Qy	1278	ATATTGAGCTGGGGGAATTTATCTAATATGATAAAAAACAACTGATTTTCAATTTCTCTGT	1337
Db	2742	TACAGCAGGATCTGGGCAATAACTTATGATGTAATAATAAATATTTTCGGGTACCAAT	2801
Qy	1338	AAAAAAGACTGTAAACCAATTAATTAATCCAAATGTTTACCAAGCTATAATAGTTATAG	1397
Db	2802	TCCTAAACGAGAGAGAAATCAAGGAACCTACCTTTTCCCAATATGATAACTATAG	2861
Qy	1398	TCATATTTTATCCAGCTTTCTTTATTTAATTAATCTCTATAAATTTGGATTAGCGCTAAA	1457
Db	2862	TCATATTTTATCATTTTATTAATAAGTCTTAGTATCCC-----TGCAACATA	2906
Qy	1458	TATATTATATACAGGTGCATTAGATGACACAGTAGTGTGTTAATAGAAATAATGCAAT	1517
Db	2907	TAAAACTCAAGTGATACGTTTCTGTTGGACACACTCTAGTGTGATGCTCTTAAAAATACAAT	2966
Qy	1518	ATCAGATAAATAATTAACAATGATCCAGCAATCAAGGTAACAGCTCTTGATACAAACTC	1577
Db	2967	TTATACACATTTAACTACCAATTCAGCTGTAAAGCGAATTCACCTGGGACTGCTTC	3026
Qy	1578	TAAGGTAAATTAAGGACCTGGTCATACAGAGGAAACTTGGTTTATTTAACAAGTCAAGG	1637
Db	3027	TAAGTTGTTTCAAGGACCTGGTCATACAGAGGAGGATTTAATGATTTCAAGATCA---	3083
Qy	1638	CGGTTTAGAGATTACATGTAGAACTCTTAATCTACACAATCTTATTACATTAGACTTCG	1697
Db	3084	---TTTCAAAAATTAACATGTCAACACTCAAAATTTTCAACAATCGTATTTTATAGAAATCG	3140
Qy	1698	ATAGCTTACAAATGGTGTGAAATATCTTCTTAAATATATCTTACAAATACAGAGAT	1757
Db	3141	TTATGCTTCAAAATGGAAGCGCAATATCTGAGCTGTATTAATCTTTAGTATCCAGGGGT	3200
Qy	1758	AATAGGAATACCACTCAACGACTCAACAACTTTTCTGGTACAAATTAATAAATTT	1817
Db	3201	AGCAGACTG---GGTATGGCACTCAACCCACATTTTCTGGTACAGATTATACGAATTT	3257
Qy	1818	ACATACGGAGATTTGGGTATTTTCCAAATTTCCAAATGATACAGTACATTAATTCG	1877
Db	3258	AAAATATAAGATTTTTCAGTACTTAGAATTTTCTTAACGAGGTGAAATTTGCTCCAAATCA	3317
Qy	1878	AAACATACATTTATATTTATTCGTGCGAGATGAT---CAAATTCAAATTTTAAATCATGA	1934
Db	3318	AAACATATCTCTGTGTTTAAATCGTTCGGATGATATACAAACACACAGTACTTATGA	3377
Qy	1935	TAAATTTGAAATTTATACCAATTTACTTCTCTGTAGCCAAATTAAGAGAAAAACAAAAT	1994
Db	3378	TAAATTTGAAATTTCTGCCAATTTACTCTGTTTCTAATAGAGAGGATAGAGAGAAACAAAAT	3437
Qy	1995	AGAACTATCCAAACAAAATAAATAATATATTTTTCATAAATCATACAAAAATACCTTTAA	2054

3438

AGAAACAGTACAAACAAATAATTAATACATTTTATGCAAAATCTTATAAAAAACACTTTTACA

3497

2055

TATAGAACCCACAACTATGATATTGATTAA

2085

3498

ATCAGAACTTACAGATTATGACATAGATCAA

3528

AAQ14669

standard; DNA; 3543 BP.

AAQ14669

27-AUG-2003

(revised)

25-MAR-2003

(revised)

04-FEB-1992

(first entry)

Dipteran active toxin gene.

Insecticide; B.t; crystal; delta endotoxin; cryIIA; ss.

Bacillus thuringiensis serovar morrisoni.

Key

Location/Qualifiers

CDS

1..3543

/*tag= a

EP457498-A.

21-NOV-1991.

09-MAY-1991;

91EP-00304180.

15-MAY-1990;

90US-00524255.

01-OCT-1990;

90US-00590903.

(MYCO) MYCOGEN CORP.

Sick AJ;

WPI; 1991-341902/47.

P-PSDB; AAR14373.

Bacillus thuringiensis genes encoding diptera-active toxins - and transformed microbes used to control insects in various environments.

Claim 1; Page 10; 20pp; English.

The sequence was obtd. from plasmid pMYC1625 which was isolated from a genomic library prepd. from DNA from B.t. PS71M3 [from B.t. PS71M3-69 (NRRL B-18515)]. It is related to the cryIIA family of genes, the 140 kD endotoxin gene and the type II gene from B.t. var. israelensis. The gene encodes a 130 kD protein. Microorganisms transformed with the DNA may be administered to dipteran insects or their environments, the expressed toxins acting as an insecticide. See also AAQ14670-Q14672. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)

Sequence 3543 BP; 1278 A; 567 C; 612 G; 1086 T; 0 U; 0 Other;

Query Match

15.9%; Score 331.4; DB 2; Length 3543;

Best Local Similarity

53.8%; Pred. No. 3.7e-46;

Matches 856; Conservative 0; Mismatches 697; Indels 38; Gaps 7;

Qy

499

TATAAAAACGCTATTACTACCTATTATGCGCAAGCTGCTTAATTTTCAATTTTAAATTTATTA

558

Db

604

TATAACATACATAGTATTATCTAGTTATGCAACGACGACAACTTACATCTGACTGTATTA

663

Qy

559

CAACAGGTGCTGAATTTGGCTGATGATGGAATGCAGATATACATCTTCACAAATTTGAA

618

Db

664

AATCAAGCCGTCAAATTTGAAGCGGTATTTAAAAAACAAATCGCAATTCGATTTATTAGAG

723

Qy

619

CCTAATCTGGAACATCAGATGACTATTATAAACTTTTAAAAAGAAATATACCTAAATAT

678

Query Match		15.9%;	Score 331.4;	DB 2;	Length 3543;
Best Local Similarity		53.8%;	Pred. No. 3.7e-46;	Indels 38;	Gaps 7;
Matches 856;		Conservative	0;	Mismatches 697;	
QY	499	TATAAAACGCTATTACTACCTATTTATGGCAGCTGCTAAATTTTCATTTAATTTATTA	558		
DB	604	TATACATCTAGTATTAICTAGTTATGCACAGCAGCAAACTTACATCTGACTGTATTA	663		
QY	559	CAACAGGCTGCTGAATTTGGCTGATGAATGGAATGCGAGATATACATCCTTCACAAATGAA	618		
DB	664	AATCAAGCCGTCAAATTTGAAGCGTATTTAAAAAACAAATCGACAATTCGATTTTAGAG	723		
QY	619	CCTAATGCTGGACATCAGATGACTATTAATACTTTTAAAGAAATATACCTAAATAT	678		
DB	724	CCTTTGCC---AACAGCAATTTGATTTATTCAGTATTTGACTAAAGCTATGAAGATTAC	780		
QY	679	AGTAACCTATTGTGCAAAATCCTATAGAGAGAGCTAAATAAACTTCGAAACGACCTAAT	738		
DB	781	ACTAATATTGTGTACAACTTATATAAAGAGTAAATTTTAAATTAACGACGCTGAT	840		
QY	739	ATGAGATGGAGTATATTTAATGATATTCGAAGATATATGACTATTTACTGTATTAGACT	798		
DB	841	AGTAATCTTGATGAAATATAAACTTGAACACATACATACTGATTCGAAACAAAATGACT	900		
QY	799	ATCGCTCAATTTCTTTTATGATATAAAGAGATACAAAGATTCATAGGAGAAATAGGT	858		
DB	901	ACTGCTGATTTAGATCTTGTGCACTCTTTCTTAATTTATGATGTAGGTAAATATCCAATA	960		
QY	859	GGCATTAAATCACTCAACAGAAATTTATACAACTGAAATAAATTTTGACCGCTTT	918		
DB	961	GGTGTCCAACTGAACTTACTCGAATAATTTAT-----CAGTACTTAACCTCGAAGA	1013		
QY	919	ACTTACCTTGAAATTCACCCAACTCTGCTATATATGGAATATATATTTAACACGTTACGG	978		
DB	1014	AAGCCCTATAAATATTATGACTTTTCAATATCAAGAGGATTCATTTACAGGTAGACGCA	1073		
QY	979	CTTAGATATTTTCAATTTTATGATGAATTTATTTATACAAAATGAAAGTACGGG	1038		
DB	1074	TTTATTTACTTGGCTTGATTTCTTTGAATTTTATGAAAAAGCGCAAACTACTCTTAATAA	1133		
QY	1039	AATCGTTTGTGTTGGAATTCGTAATAGATCTACTTT-ATGCTACGACAGGAACTGA	1097		
DB	1134	TTTTTTCACAGCCATTAATAATGTTTTCATTACACACTTGTATTAATATATCCCAAAATC	1193		
QY	1098	AATATATATGGAAGAAAGACAGGTCCACCACACAAAAAACTTTAATACATTTGAATC	1157		
DB	1194	TAGTGTTTTGGAAATCACAATGTAACTGTATAATTAATAATCTCTGTTTGGCAACAA	1253		
QY	1158	CTATAAAGTTTCAATGTAATGTAAGACAGTAACCTCTACTTCCCTTTTCTTAACAT	1217		
DB	1254	TATTTATATTTTATTAATAATGTACAAAGCTTAGATAATAAATATCTAAATGATTATAA	1313		
QY	1218	ATACTTTACAAATTAATCAATTTGAACCTTTATTTAATAATTCACCTAGTAATAAATAAC	1277		
DB	1314	TAATATTAGTAAATGGAATTTTATTAACATAATGTTAGTACTAGACTTTTGGHGAAGAAT	1373		
QY	1278	ATATTACAGCTGGGGGAATTTATCTAATGATATAAAAAACAACTGATTTTCAATTTCCCTGT	1337		
DB	1374	TACAGCAGGATCTGGGCAATAAATCTTATGATGTAATAAATAATTTTTCGGGTTACCAAT	1433		
QY	1338	AAAAAAGAGCTGTAACCAATTAATAATCCAAATGTTTACCAAGCTATATAATAGTTATAG	1397		
DB	1434	TCCTTAACCAAGAGAGAATCAAGCAATCCCTACCCCTTTTTCCAACATATGATACTATAG	1493		
QY	1398	TCATATTTTATCCAGTTTCTTTTATTTAATTTTCTTATAAATTTGGATTAGCGCTAAA	1457		
DB	1494	TCATATTTTATCATTTTATTAAGAAGTCTTTAGTATCC-----TGCAACATA	1538		
QY	1458	TATATTATACAGGTGCTATTAGGATGGACACACAGTAGTGTGTTAATAGAAATAATGCAAT	1517		
DB	1539	TAAACTCAAGTGTATAGTTTGTGCTTGGACACACACTCTAGTGTGATCTCTAATAATACAA	1598		
QY	1518	ATCAGATAAATAAATTAACAATGATCCAGCAATCAAGGTAAACAGTCTTGTATACAAACTC	1577		
DB	1599	TTATACACATTTAACTACCCAAATTTCCAGCTGTAAAAAGCGAAATTCATTTGGGACTCTTC	1658		
QY	1578	TAAGTAAATTAAGNACCTGTCATACAGGAGGAACTTTGGTTTATTTTACAAAGTCAAGG	1637		
DB	1659	TAAGGTGTGTTCAAGGACCTGGGTATACACAGGAGGGGATTTAAATTTGATTTCAAGATCA	1715		
QY	1638	GGTTTATAGAGATTACATGTAGAACTCCTAATTTCTACACAATCTTTATACATTAGACTTCG	1697		
DB	1716	---TTTCAAAATTTACATGTCACACCTCAAAATTTTCAACATCTGTATTTATAAGAAATTCG	1772		
QY	1698	ATACGCTCAAAATGGTGTGGAATACTCTTCTTAATAATATCTCTTCAATATACAGAGT	1757		
DB	1773	TTATGCTTCAAAATGGAAGCGCAAAATACAGAGCTGTTATAAAATCTTAGTATCCAGGGG-	1831		
QY	1758	AATAGAAATACCACCTCAACGACTCAACACACTTTTCTGCTGACAAAATTTATAATAATTT	1817		
DB	1832	--TAGCAGAACTGGGTATGGCACTCAACCCCACTTTTCTGCTGACAGATTTATAGAAATTT	1889		
QY	1818	ACAATACGGAGATTTTGGGTATTTTCCAAATTTTCCAACTACAGTAACATTTACCTTTAAATCG	1877		
DB	1890	AAATATAAAGATTTTTCAGTACTTAGAATTTTCTAACGAGGTGAAATTTTCTCCAAATCA	1949		
QY	1878	AAACATACCATTTTATATTTAATCGTGCAGATGAT---CAAATTCATTTTATCATTTGA	1934		
DB	1950	AAACATATCTTGTGTTTAAATCGTTTCGGATGTATATACAAACACACACAGTACTTATGA	2009		
QY	1935	TAAATTTGAATTTATACCAATTTACTTCTCTGTACGCCAAATAGAGAAAAACAAAAATTT	1994		
DB	2010	TAAATTTGAATTTTCTGCCAATTTACTCTGTTCTATAGAGAGGTAGAGAGAAACAAAAATTT	2069		
QY	1995	AGAACTATCCAAACAAAAATAATACATTTTTCACAAATCATACAAAAAATACCTTTAAA	2054		
DB	2070	AGAAACAGTACAAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2129		
QY	2055	TATAGAGGCCCAAACTATGATATTGATTA	2085		
DB	2130	ATCAGAACTTACAGATTTATGACATAGATCA	2160		
RESULT 9		AAD43974			
ID	AAD43974	standard; DNA; 4896 BP.			
XX	AC	AAD43974;			
XX	DT	13-DEC-2002 (first entry)			
XX	DE	Bacillus thuringiensis ssp. finitimus cry28Aa1 gene.			
XX	KW	Delta-endotoxin; cry26Aa1; cry28Aa1; insect-resistant plant; toxin;			
XX	OS	transgenic host cell; insecticide; gene; db.			
XX	FT	Bacillus thuringiensis.			
XX	FT	Key Location/Qualifiers			
XX	FT	CDS 1129..4458			
XX	FT	/*tag= a			
XX	FT	/product= "cry28Aa1 gene"			
XX	PN	US2002038005-A1.			
XX	PD	28-MAR-2002.			
XX	PF	08-JAN-2001; 2001US-00756526.			
XX	PR	07-JAN-2000; 2000US-0175158P.			
XX	PA	(WOJC/) WOJCIECHOWSKA J A.			
XX	PA	(LEWI/) LEWITIN E I.			
XX	PA	(ZALU/) ZALUNIN I A.			
XX	PA	(REVI/) REVINA L P.			
XX	PA	(CHES/) CHESTUKHINA G G.			

XX	Wojciechowska JA, Lewitin EI, Zalunin IA, Revina LP;	690	TGCAATACCTATAGAGGAGGACTAATAAACTTCGAACGACACCTAATATGAGATGGAG	749
PI	Chestukhina GG;	1788	CACCAAGACATACCATAAAGGATTGAATCACCCTTAAAGAAATCAGAAAATCACATGGGA	1847
XX				
DR	WPI; 2002-403936/43.	750	TATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATFACCTATCGCTCAATT	809
XX	P-PSDB; AAE26353.	1848	TGCTTATACACATATCGTCGAGAATGACCTTAATTGTATTGGATCTTGTGCGCACTTT	1907
PT	Novel isolated delta-endotoxin nucleic acid molecules, cry26Aa1 and			
PT	cry28Aa1 isolated from Bacillus thuringiensis finitimus, that encodes			
PT	toxin active against insects, useful for controlling insects.			
PS	Claim 1; Page 33-37; 42pp; English.			
XX	The invention relates to isolated delta-endotoxin nucleic acid molecules,			
CC	cry26Aa1 and cry28Aa1 isolated from Bacillus thuringiensis finitimus,			
CC	that encode a toxin that is active against insects. The invention is			
CC	useful for producing an insect-resistant plant, by introducing the			
CC	nucleic acid molecule into the plant, where the nucleic acid is			
CC	expressible in the plant in an effective amount to control an insect. The			
CC	invention is useful for producing a toxin that is active against insects			
CC	by obtaining the transgenic host cell and expressing the nucleic acid			
CC	molecule in the host cell, which results in the toxin that is active			
CC	against insects. The toxin is useful for controlling an insect by			
CC	delivering to the insect an effective amount of toxin. The invention is			
CC	useful for controlling insects. The toxin is useful for inhibiting the			
CC	ability of insect pest to survive, grow or reproduce, for limiting insect			
CC	-related damage or loss in crop plants, and to prophylactically treat			
CC	insect susceptible areas or plants to confer protection or resistance			
CC	against harmful insects. The present sequence is Bacillus thuringiensis			
CC	spp. finitimus cry28Aa1 gene			
XX				
SQ	Sequence 4896 BP; 1727 A; 757 C; 887 G; 1525 T; 0 U; 0 Other;			
Query Match 7.7%; Score 161.2; DB 6; Length 4896;				
Best Local Similarity 57.0%; Pred. No. 8.9e-18;				
Matches 385; Conservative 0; Mismatches 243; Indels 48; Gaps 3;				
QY	153 AGGTGCTATAATAATCTTTTGGTACCTCAATCACTGCTTTTGGCCCGGGGAGAAC	212		
Db	1293 AGGTGGTGACTATATATCATCTTGGAACTTGGCTCCCGTCTTTGGCCCTGATCCAGAGA	1352		
QY	213 AGA---CAAAACAGATGACACAAATTTATTAATGGGAGAAATTTTGTGTATACAC	269		
Db	1353 AGATCAAAAAAATTTGTGTCAATTTATGAACACGGAGAGACCTTTTAATCAAC	1412		
QY	270 GTTAAACAGAAAGCATAAAAACAGCTAAAGTTACAAAATTTAGAGGATTTAGACAAATAT	329		
Db	1413 AATTTCTACAGCTGTAAGAAGAAATAGCATTAGCTCAATGGTTTAAAGATGTATT	1472		
QY	330 ACAAGCTATAATACAGCAATTAGATGGAGAAAATTTAAAGACTACAAGCTCCTGG	389		
Db	1473 AACGTACTATGAAGAGCAATTTAATGATTGGAGAGAAATCCAAGTGCAAATACTGCCAG	1532		
QY	390 ATTACCACTATCATCAGCATTAACAACAGCTGCTTGACTCTTAAATACGATTTGAGAA	449		
Db	1533 ATTGGTATCACAGA-----GATTTGAAA	1556		
QY	450 TGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACCTTGAACCTTATAAAACGCT	509		
Db	1557 CGTCAATTCATTTTGTAAAGCAATATGCCAACTCCAACCTTCCACGATATGACACATT	1616		
QY	510 ATTACTACCTTATATGCCCAAGCTGCTAATTTTCATTTTAATTTATTAACAACAGGTGC	569		
Db	1617 ATTATTAAAGTTGCTATACAGAAAGCTGCAAAATTTACATTTTGAATTTATTAACATCAAGGTG	1676		
QY	570 TGAATTTGGCTGATGAATGAAGTCACATATACATCTTCCAAAATTTGAACCTTAATGCTCG	629		
Db	1677 ACAATTCGGGATCAATGGAATGCAGATCAACACATTCACCAAT-----GTTGNA	1727		
QY	630 AACATCAGATGACTATTATAAACTTTTAAAGAAATAATATACCTTAATAATAGTAACCTATTG	689		
Db	1728 GTCATCAGGTACTTATTATGACGAGCTATTGGTATATATTGAAAGATATATTAATATTG	1787		
QY	690 TGCATACCTATAGAGGAGGACTAATAAACTTCGAACGACACCTAATATGAGATGGAG	749		
Db	1788 CACCAAGACATACCATAAAGGATTGAATCACCCTTAAAGAAATCAGAAAATCACATGGGA	1847		
QY	750 TATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATFACCTATCGCTCAATT	809		
Db	1848 TGCTTATACACATATCGTCGAGAATGACCTTAATTGTATTGGATCTTGTGCGCACTTT	1907		
QY	810 TTCCTTTTATGATATA 825			
Db	1908 TCCTTTTATGATATA 1923			
RESULT 10				
ADF31301				
ID	ADF31301 standard; DNA; 4896 BP.			
AC	ADF31301;			
XX	12-FEB-2004 (first entry)			
DT	Bacillus thuringiensis serovar finitimus pF2 DNA clone.			
DE	Cry26Aa1; cry28Aa1; delta-endotoxin; insect pest control;			
XX	transgenic plant; insect resistance; insecticide; gene; ds.			
KW	Bacillus thuringiensis serovar finitimus.			
OS				
Key	Location/Qualifiers			
FT	1129..4458			
CDS	/*tag= a			
FT	/product= "Cry28Aa1 delta-endotoxin protein"			
XX	US2003150018-A1.			
PN	07-AUG-2003.			
XX	15-JAN-2003; 2003US-00345020.			
PF	07-JAN-2000; 2000US-0175158P.			
XX	08-JAN-2001; 2001US-00756526.			
PR	(WOJC/) WOJCIECHOWSKA J A.			
XX	(LEWI/) LEWITIN E I.			
PA	(ZALU/) ZALUNIN I A.			
PA	(REVI/) REVINA L P.			
PA	(CHES/) CHESTUKHINA G G.			
XX	Wojciechowska JA, Lewitin EI, Zalunin IA, Revina LP;			
PI	Chestukhina GG;			
XX	WPI; 2003-897623/82.			
DR	P-PSDB; ADF31302.			
XX	New isolated nucleic acid molecule encoding a toxin that is active			
PT	against insects useful for controlling insect pests or for conferring			
PT	insect resistance in plants.			
XX	Claim 7; SEQ ID NO 3; 42pp; English.			
PS	The present invention relates to the isolation of novel cry26Aa1 and			
CC	cry28Aa1 delta-endotoxin genes from Bacillus thuringiensis spp.			
CC	finitimus. The sequences for the delta-endotoxin polypeptides are also			
CC	disclosed. The invention provides methods for producing the toxins and			
CC	compositions containing the toxins. The methods and sequences of the			
CC	invention are useful for controlling insect pests in transgenic plants to			
CC	confer insect resistance. The present sequence represents a DNA clone			
CC	that contains the coding sequence for cry28Aa1 delta-endotoxin.			
XX	Sequence 4896 BP; 1727 A; 757 C; 887 G; 1525 T; 0 U; 0 Other;			
SQ	Query Match 7.7%; Score 161.2; DB 10; Length 4896;			
	Best Local Similarity 57.0%; Pred. No. 8.9e-18;			

Matches 385; Conservative 0; Mismatches 243; Indels 48; Gaps 3;
QY 153 AGGTGCTATAATAATCTTTTGGTACCTTAATCACTGTCTTTGGCCCGGGGAGAACA 212
DB 1293 AGGTGGTACTTATATCTTTGGAACTTGGCTCCGTTCTTTGGCTGTATCCAGAGGA 1352
QY 213 AGA---CAAACAGTAGTGGACAAATTTATTAATGGGAGAAATTTTGGTGTATACACC 269
DB 1353 AGATCCAAAATAAATTTGGTCAAAATTTATGAACACGGGAGAAAGCTTTTAAATCAAC 1412
QY 270 GTTAAACAGAAAGCATAAACAGCTAAAGTTTCAAACTTTTGAAGGATTTTACACAAATATT 329
DB 1413 AATTTCTACAGCTGTAAGAAGATAGCATTTAGCTCTCTAAATGGTTTAAAGATGATT 1472
QY 330 ACAAAGCTATAATACAGCATTTAGATTTGGAGAAATTTAAAGACTTACAAAGCTCTGG 389
DB 1473 AACGTACTATGAAGAGCAATTTAATGATTGGAAGAGAAATCCAAAGTGCMAATATCTGCAG 1532
QY 390 ATTACACCATCATCAGCATTAACAACAGCTGCTTGAATCTTTAAATATAGATTGAGAA 449
DB 1533 ATTGGTATCAAGA-----GATTTGAAAA 1556
QY 450 TGTTCACAAATGATTTATTCGAGAAATACCTGGTTTCCAACTTTGAAACTTTATAAAGCCT 509
DB 1557 CGCTCATTTCAATTTGTAAAGCAATATGCCAACTTCCCAAGTATGACATTT 1616
QY 510 ATTACTACCTATTATTCGCAAGCTGCTAAATTTTCAATTTTAAATTTATTAACAAGGTGC 569
DB 1617 ATTATTAAGTTGCTATACAGAGCTGCAAAATTTTCAATTTTAAATTTATTAACAAGGTGT 1676
QY 570 TGAATGGCTGATGAATGGAATGAGATATACATCTTCAAAATTTGAACCTAATGCTGG 629
DB 1677 ACAATTCGCGATCAATGGAATGAGATCAACCAATTCACCAAT-----GTTGAA 1727
QY 630 AACATCAGATGACTATTATTAATCTTTTAAAGAAATATACCTAAATATAGTAACTATTG 689
DB 1728 GTCATCAGGACTTATTATGACGAGCTTTGGTATATATTGAAAGTATATTAATATTG 1787
QY 690 TGCAAAATACCTATAGAGAAAGACTTAAATAAATCTTGAAGAAAGCACTAATATGAGATGGAG 749
DB 1788 CACCAAGACATACCAATAAGGATTTGAATCACTTTAAAGAAATCAGAAAAATCAGATGGGA 1847
QY 750 TATATTTAATGATTTATCGAAGATATATGATTTACTGTTATGATATGATATGCTCAATT 809
DB 1848 TGCTTATAACACATATCGTCGAGAAATGACCTTAATTTGTTATGATCTTGTGCAACTTT 1907
QY 810 TTCTTTTATGATATA 825
DB 1908 TCCTTTTATGATATA 1923

RESULT 11

ADP31306
ID ADP31306 standard; DNA; 4896 BP.
XX AC ADP31306;
XX AC
XX AC
DT 12-FEB-2004 (first entry)
XX DE Bacillus thuringiensis serovar finitimus pF2 DNA clone.
XX DE
XX KW Cry26Aa1; cry28Aa1; delta-endotoxin; insect pest control;
XX KW transgenic plant; insect resistance; insecticide; gene; ds.
XX OS Bacillus thuringiensis serovar finitimus.
XX FH Location/Qualifiers
XX CDS 1129..4458
FT /*tag= a
FT /product= "Cry28Aa1 delta-endotoxin protein"
XX PN US2003154510-A1.
XX XX

14-AUG-2003.
XX PF 15-JAN-2003; 2003US-00342821.
XX PR 07-JAN-2000; 2000US-0175158P.
XX PR 08-JAN-2001; 2001US-00756526.
XX PA (WOJC/) WOJCIECHOWSKA J A.
XX PA (LEWI/) LEWITIN E I.
XX PA (ZALU/) ZALUNIN I A.
XX PA (REVI/) REVINA L P.
XX PA (CHES/) CHESTURKHINA G G.
XX PI Wojciechowska JA, Lewitin EI, Zalunin IA, Revina LP;
XX PI Chestukhina GG;
XX DR WPI; 2003-897757/82.
XX DR P-PSDB; ADF31307.
XX PT New delta-endotoxin nucleic acid molecules, cry26Aa1 and cry28Aa1, useful
XX PT for controlling insect pests and for conferring insect resistance.
XX PS Claim 7; SEQ ID NO 3; 42pp; English.
XX CC The present invention relates to the isolation of novel cry26Aa1 and
XX CC cry28Aa1 delta-endotoxin genes from *Bacillus thuringiensis* ssp.
XX CC finitimus. The sequences for the delta-endotoxin polypeptides are also
XX CC disclosed. The invention provides methods for producing the toxins and
XX CC compositions containing the toxins. The methods and sequences of the
XX CC invention are useful for controlling insect pests in transgenic plants to
XX CC confer insect resistance. The present sequence represents a DNA clone
XX CC that contains the coding sequence for cry28Aa1 delta-endotoxin.
XX CC
XX SQ Sequence 4896 BP; 1727 A; 757 C; 887 G; 1525 T; 0 U; 0 Other;
Query Match 7.7%; Score 161.2; DB 10; Length 4896;
Best Local Similarity 57.0%; Pred. No. 8.9e-18;
Matches 385; Conservative 0; Mismatches 243; Indels 48; Gaps 3;
QY 153 AGGTGCTATAATAATCTTTTGGTACCTTAATCACTGTCTTTGGCCCGGGGAGAACA 212
DB 1293 AGGTGGTACTTATATCTTTGGAACTTGGCTCCGTTCTTTGGCTGTATCCAGAGGA 1352
QY 213 AGA---CAAACAGTAGTGGACAAATTTATTAATGGGAGAAATTTTGGTGTATACACC 269
DB 1353 AGATCCAAAATAAATTTGGTCAAAATTTATGAACACGGGAGAAAGCTTTTAAATCAAC 1412
QY 270 GTTAAACAGAAAGCATAAACAGCTTAAAGTTTCAAACTTTTGAAGGATTTTACACAAATATT 329
DB 1413 AATTTCTACAGCTGTAAGAAGATAGCATTTAGCTCTCTAAATGGTTTAAAGATGATT 1472
QY 330 ACAAAGCTATAATACAGCATTTAGATTTGGAGAAATTTAAAGACTTACAAAGCTCTGG 389
DB 1473 AACGTACTATGAAGAGCAATTTAATGATTGGAAGAGAAATCCAAAGTGCMAATATCTGCAG 1532
QY 390 ATTACACCATCATCAGCATTAACAACAGCTGCTTGAATCTTTAAATATGACATTGAGAA 449
DB 1533 ATTGGTATCAAGA-----GATTTGAAAA 1556
QY 450 TGTTCACAAATGATTTATTCGAGAAATACCTGGTTTCCAACTTTGAAACTTTATAAAGCCT 509
DB 1557 CGCTCATTTCAATTTGTAAAGCAATATGCCAACTTCCCAAGTATGACATTT 1616
QY 510 ATTACTACCTATTATTCGCAAGCTGCTAAATTTTCAATTTTAAATTTATTAACAAGGTGC 569
DB 1617 ATTATTAAGTTGCTATACAGAGCTGCAAAATTTTCAATTTTAAATTTATTAACAAGGTGT 1676
QY 570 TGAATGGCTGATGAATGGAATGAGATATACATCTTCAAAATTTGAACCTAATGCTGG 629
DB 1677 ACAATTCGCGATCAATGGAATGAGATCAACCAATTCACCAAT-----GTTGAA 1727
QY 630 AACATCAGATGACTATTATTAATCTTTTAAAGAAATATACCTAAATATAGTAACTATTG 689

Db	1728	GTCAATCAGGCTACTTATTATGACGAGCTATTGGTATATATTGAAAAAGTATATTAAATTATTG	1787
Qy	690	TGCAAAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAAACCTTAATATGAGATGGAG	749
Db	1788	CACCAAGACATACCATAAAGGATTGAATCACCTTAAAGAAATCAGAAAAAATCACATGGGA	1847
Qy	750	TATATTTAATGATTATCGAAGATATATGACTATTACTGTATTATTAGATACATATCGTCAATT	809
Db	1848	TGCTTTATAACATATCGTCGAGAAATGACCTTAATTGTATTGGATCTTGTGCGCACTTT	1907
Qy	810	TTCTTTTATGATATA	825
Db	1908	TCCTTTTATGATATA	1923
RESULT 12			
ID	AAQ14670		
XX	AAQ14670	standard; DNA; 2061 BP.	
AC	AAQ14670;		
XX			
DT	27-AUG-2003	(revised)	
DT	25-MAR-2003	(revised)	
DT	04-FEB-1992	(first entry)	
XX			
DE	Dipteran active toxin gene.		
XX	Insecticide; B.t; crystal; delta endotoxin; cryIVC; ss.		
KW			
XX			
OS	Bacillus thuringiensis serovar morrisoni.		
XX			
FH	Key	Location/Qualifiers	
FT	1.	2028	
FT	/*tag= a		
XX			
PN	EP457498-A.		
PD	21-NOV-1991.		
XX			
PF	09-MAY-1991;	91EP-00304180.	
XX			
PR	15-MAY-1990;	90US-00524255.	
PR	01-OCT-1990;	90US-00509093.	
XX			
PA	(MYCO) MYCOGEN CORP.		
XX			
PI	Sick AJ;		
XX			
DR	WPI; 1991-341902/47.		
DR	P-PSDB; AAR14374.		
XX			
XX	Bacillus thuringiensis genes encoding diptera-active toxins - and transformed microbes used to control insects in various environments.		
PT			
PT			
XX			
PS	Claim 1; Page 15; 20pp; English.		
XX			
CC	The sequence was obtd. from plasmid pMYC1636 which was isolated from a genomic library prepd. from DNA from B.t. PS71M3 [from B.t. PS71M3-69 (NRRL B-1815)]. It is related to the cryIVC from B.t. var. israelensis. The gene encodes a 77 kD protein. Microorganisms transformed with the DNA may be administered to dipteran insects or their environments, the expressed toxins acting as an insecticide. See also AAQ14669-Q14672. (updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)		
XX			
SQ	Sequence 2061 BP; 779 A; 331 C; 319 G; 632 T; 0 U; 0 Other;		
Query Match 7.6%; Score 158; DB 2; Length 2061;			
Best Local Similarity 48.3%; Pred. No. 3e-17;			
Matches 999; Conservative 0; Mismatches 895; Indels 174; Gaps 13;			
Qy	2	TCGTGTCAGGGGAATACACAATATGGTGATAATTTTCGAGACATTTGCTAGTGTGATACAA	61

149	TGTGTCAGAGATAATCAACAATATGCGCAATAATGCGGGAATTTTGTAGTCTGTAACACTA	208
62	TTGCTGCAAGTTAGTCAGGTACTATTCTATCGGTACTCTGTAGCCGTATAGGTGGC	121
209	TTGTTGGAGTTAGTCAGGTATTATTGTAGTAGGAACTATGTTAGGAGCTTTTGCTGCC	268
122	TCACCTTCTATATCCGGACCGATAGGAATAATAGGTGCTATATAATAATATCTTTTGGTACC	181
269	-----CTGCTTAGCTGCGAGTATATACTTTTGGACTT	304
182	TAATCACTGTCTTTTGGCCCGGGAGAACAGACAAACAGTATGGAACACAATTTATTA	241
305	TGTTGCCGATCTTTTGGCAAGGATCTGACCCCTG---CAAATGTTGGCAGGATTGTGTA	361
242	AAATGGGAGAAATTTTGTGATACACCGTTAACAGAAAGCATAAACAGCTAAAGTTAC	301
362	ACATCGGAGGAGGCTATACAGAAATAGATAAAACATATAATTAATGACTAACTT---	418
302	AAACTTTAGAGGATTTAGACAAATATTACAAAGCTATAATAACAGCATTAGATGGA	361
419	---CTATCGTAAACCTTATAAAATCACTTGATTAATAATCAAGATTTTCGATAAAT	475
362	GAAATTTAAAGACTACAAGCTCCTGGATTACCAACCATCATCAGCATTTACAAACAGCTG	421
476	GGAGCCAGCAGGTACACACGCTAATGCTAAAGCAGTA-CATGATCTCTTTACTACCTTA	534
422	CCTTGACTCTTAAATACGATTTGAGAAATGTTCACAATGATTTTATTCGAGAAATACCTG	481
535	GAACTATAATAGATAAAAGATTTAGATATGTTAAAAA-----	571
482	GTTCCTCAACTTGAAACTTTATAAACGCTATTACTACTATTATTCGCGAAGCTGCTAAAT	541
572	-----ATAATGCTAGCTATCGAATACCAACACTCCCTGCATATGCACAAATAGCTACTT	625
542	TTCAATTTAAATTTATTACAACAAGGTGCTGAAATTCGGCTGATGAATGGAATCGAGATATAC	601
626	GGCACTTGAAATTTATTAAACCATGCTGCTACCTATTACAATATATGGCTGCAAAATCAAG	685
602	ATCCTTCAAAATTTGAACCTTAATGCTGGAAACATCAGATGACTATTATAAATTTTAAAG	661
686	GT-----ATAAATCCAAGTACTTTCAATTCATCTAATTAATTAATCAGGCTATTATAAAC	739
662	AAATATACCTAAATATAGTAACCTATTGTGCAATACCTATAGAGAAGGACTTAAATAAAC	721
740	GTAATAATACAGAAATATGACTATTGTATACAAACGTACAAATGCGAGCTAACTATGA	799
722	TTCGAAACGAACCTTAATAGATGGAGTATATTAAATGATTTATCGAAGATATATGACTA	781
800	TTAGAACTAATACTATAACGAACATGGAATATGTAATAATACTTTACCGTTTATAGAAATGACTC	859
782	TTACTGTATTAGATACTATCGCTCAATTTTCTTTTATGATATTAAGAGATACAAAGATT	841
860	TAACTGTGTTAGATCTTATTGCTATTTTCCAAATTAATGACCAGAAAAATA-----	911
842	CAATAGGAAGAATAGGTGGCTATTAACACTTGAACCTTACAAGAGAAAAATTTATACAAC	901
912	-----TCCAATAGAGTTAAATCTGAACCTTACCAGAGAAGTTTATACGAATGTTA	961
902	TAAATTTTGACCGTCTTACTTACCTTTGAAATTCACCCCAATTCGCTATAATATGGAATATA	961
962	-----ATTCAGATACATTTTAGAACCATTAACAGAACTAGAAA	997
962	ATTTHAACAGTTTCAGGGCTTAGATTTATTTTCATTTTATAGATCACTTATATTTTATACAA	1021
998	ATGGATTAACTAGAAATCCTACATTTATTACTTTGGATTAACCAAGGCGCTTTTACACAA	1057
1022	AAATGAAACGCTACGGGAATCGTTTAGTTGGTATTTGCGAATCGTAATAGATCTTACTATG	1081
1058	GAAATCTCGAGACATTTCTGATCCTTATGATATTTCTTTTACAGGTAAACAGATGG	1117
1082	CTACGACAGGAACCTGAAATTTATATATGAGAGAAAGAACAGGTCCACCCACAAACAAACTT	1141
1118	CCTTTTACACATACTAATGATGATCGCAACATAATCTGGGGAGCGGTTTCTATGGACATATTA	1177

1142 TAATACCAATTTGAATCCTATAAAGTTTCAATTTGTAATCTGATAGACAAAGTAATCCTACTT 1201
1178 TTTCTCAAGACACATCCAAAGTATTTCCCTTTTATAGAAACAAACCTATTGTATAAGGTGCG 1237
1202 CCCCTTTTCTCAACATATACCTTTACAAATTAATCAAAATTCGAACCTTTATTTAAATAATTTAC 1261
1238 AAATTGTCAGACATAGAGAGTACTCAGATATAATATATAGAAATGATATTTTTCGAATA 1297
1262 CTAGTAATAAATTAACATATTCAGCTGGGGGAATTTATCTAATGATAAAAAACAACCTG 1321
1298 GCAGTGAAGTATTTTCGATATTCATCCAAATTCACAAATAGAAAATAATTATAAAGAACTG 1357
1322 ATTTTCAATTTCTGTAAATAAAGAGCTGTAAACCAATTAATTAATCCAAATTTGTTACCA 1381
1358 ATTTCTATATGATTTCCAAAACCAACATCGAAAATAAAGAAATATGTCATCTATCTGTT 1417
1382 GCTATAATAGTTATAGTCATATTTTATCCAGTTTCTTTATTTAATTTATCTCTATAAAA 1441
1418 ATATAAAAACCTGATAATTAATATTTTC----- 1445
1442 TTGGATTAGCGCTAAATATATATATATATACAGGTGCATTAGAGTGGACACACAGTAGTTTA 1501
1446 -----AGTAGTTAGAGGAAGAAGAGTTGCAATTTAGTTGGACACATACTAGTGTG 1498
1502 ATAGAAATATGCAATATCAGATAAATAATTAATTAATGATCCAGCAATCAAAAGGTAA 1561
1499 ATTTCCAAAATACATAGATTTAGATAAATCAATCCCAAAATCCACGCTCTAAAGCTTTGA 1558
1562 GTCTTGATCAAACTCTAGGTAAATTTGAAGACCTGTGCATACAGAGGAACTCGTTT 1621
1559 AGTAAAGTTCTGATTCGAAATTTGTGAAGGTCTGTGCACAGGTGGAGCTTGGTAA 1618
1622 ATTTACAAAGTCAAGCGCTTTAGAGATTAATCATGTAGAACTCCTAAATTTTACAAATCTT 1681
1619 TTCTTAAGTAGTAGTGGATTTAGAGTTAGATTTTAAATAATGTTTCTCGCAAT--- 1675
1682 ATPACATTAGACTTCGATACGCTACAAATGGTGTGGAATATCTTCTTAATATATCTC 1741
1676 ATCAAGTACGTATTCGTTATGCTACTAATTCCTCAAGACACACAGTA--TTCTTAACCGG 1733
1742 TTACAATACAGAGTAATAGGAATACCACCTCAAGACCTCAACACACACTTTTCTTGTA 1801
1734 AATAGATACTATAAGTGTGGAGCTCCCTAGTACACTTCCCGCCAAAC-----C 1783
1802 CAAATTATAATAATTTACAATACGAGATTTTGGGTATTTCCAAATTTCCAAGTACAGT-- 1859
1784 CAAATGCTACAGATTTAAACATATGCAGATTTTGGATATGTAACATTTCCAAAGAACAGTTC 1843
1860 -----AACATTACCTTTAAATCGAAACATACCATTTATTTAATCGTGCAGATGTAT 1912
1844 CAAATAAACAATTTGAAGGAGAGACACTTTTATTAATGACCTTATATGGTACACCAATC 1903
1913 CAAATTCAAATTTAATCATGATAAATTTGAATTTATACCAATTTACTTCTGTACGCC 1972
1904 ATTCAATATATATATATTGACAAAATCGAATTTATTCGAATCACTCAATCTGTATAG 1963
1973 AAAATAGAGAAAACAAAATTTAGAACTATCCAAAACAAAATAAATACATTTTTCCAA 2032
1964 ATTTACAGAGAACAAAATATAGAAAACACAGAAAATAGTGAATGATTTATTTGTTA 2023
2033 ATCATACAAAATAATCTTTTAAATATAGA 2060
2024 ATTAACAAAGTTCTTACTAAATATAGA 2051

RESULT 13
AAQ81180
ID AAQ81180 standard; DNA; 2061 BP.

XX AC AAQ81180;

DT 25-MAR-2003 (revised)

12-AUG-1995 (first entry)
XX DE B.t. toxin PS7IM3 gene.
XX KW Delta-endotoxin; crystal protein; biological control agent; Calliphorid;
XX KW screw-worm; sheep blowfly; Lucilla; Phormia; Calliphora; insecticide;
XX KW pesticide; B.t.; ss.
XX OS Bacillus thuringiensis.
XX PN W09502694-A2.
XX PD 26-JAN-1995.
XX PF 13-JUL-1994; 94WO-US007902.
XX PR 15-JUL-1993; 93US-00093199.
XX PA (MYCO) MYCOGEN CORP.
XX PI Hickie LA, Payne J;
XX DR WPI; 1995-067338/09.
XX DR P-PSDB; AAR63079.
XX PT Method for controlling Calliphoridae pests - specifically utilises
XX PT Bacillus thuringiensis isolates or toxins.
XX PS Disclosure; Page 42-43; 50pp; English.
XX CC A library was constructed from Bacillus thuringiensis PS7IM3 total
XX CC cellular DNA in lambda Gem-11. Plasmid pMYC1636, selected in Escherichia
XX CC coli, contained a 15 kb insert expressing a beta-endotoxin gene. This was
XX CC sequenced (AAQ81180). A cured, acrySTALLIFEROUS B.t. host carrying
XX CC pMYC1636 produced a 77 kDa crystal protein (AAR63079). (Updated on 25-MAR
XX CC -2003 to correct PN field.)
SQ Sequence 2061 BP; 779 A; 331 C; 319 G; 632 T; 0 U; 0 Other;
Query Match 7.6%; Score 158; DB 2; Length 2061;
Best Local Similarity 48.3%; Pred. No. 3e-17;
Matches 999; Conservative 0; Mismatches 895; Indels 174; Gaps 13;
QY 2 TGTGTCGAAGGAATACACAAATATGTCATATTTCCAGACATTTGCTAGTCTGATACAA 61
DB 149 TGTGTCAGATATCAACAATATGCGCAATATGCGGGAATTTGTTAGTCTGAAACTA 208
QY 62 TTGCTGCAGTTAGTGCAGGTACTATTGTATCCGGTACTCTGTAGCCGGTATAGGTGGC 121
DB 209 TTGTTGGAGTTAGTGCAGGTATTATTGTAGTAGGAACATATGTTAGGAGCTTTTCTGCC 268
QY 122 TCACTTCTATATCCGGNCCGATAGGATATAGTGTCTATAATAATATCTTTTGGTACC 181
DB 269 -----CTGTCTTAGCTGCAGGTATAATATCTTTTGGACTT 304
QY 182 TAATCACTGTCTTTTGGCCGCGGAGAACACAGACAAACAGATATGGACACAAATTTATTA 241
DB 305 TGTGTCGATCTTTTGGCAAGGATCTGACCTG---CAAATGTTTGGCAGGATTTGTTAA 361
QY 242 AAATGGGAGAAAATTTTGTGATACACCGTTTAAACAGAAAGCATAAAACAGCTAAGTTAC 301
DB 362 ACATCGGAGGAGCCCTATACAGNAATAGATAAAAACATAAATTAATGTACTACTT--- 418
QY 302 AAATTTAGAGGATTTAGACAAATATTAACAGCTATATAACAGCTATAGATGATTTGA 361
DB 419 ---CTATCGTAACACCTTATAAAAAATCACTTGAATAATCAAGAATTTTTCGATAAT 475
QY 362 GAAATTTAAAAGACTCAAGCTCCTGGATTACCACCATCATCAGCATTAACAAGAGCTG 421
DB 476 GGGAGCCAGCAGCTACACAGCTAATGCTAAAGCAGTA-CATGATCTCTTTTACTACCTTA 534
QY 422 CCTTGACTCTTAAATACGATTTTGAGAAATGTTCAATGATTTTATTCGAGAAATACCTG 481

Db 535 GAACCTATTAATAGATAAGATTAGATATGTTAAAAA----- 571
Qy 482 GTTTCCAACTTGAACCTTATAAAGCTATTACTACCTATTTATCGCGAAGCTGCTAATT 541
Db 572 -----ATAATGCTAGCTATCGAATACCAACACTCCCTGCATATGCACAAATAGCTACTT 625
Qy 542 TTCAATTAAATTTATACAAAGGCTGTAATTTGGCTGATGAATGGAATGCAGATATAC 601
Db 626 GGCACCTGAATTTATTAACAACATGCTGCTACCTATTAACAATATATGGCTGCAAAATCAAG 685
Qy 602 ATCCCTTCAAAATTGAACCTTAATGCTGGAAACATCAGATGACTATTATAAACTTTTAAAG 661
Db 686 GT-----ATAATCCAGTACTTTCAATTCAATTAATTAATCAAGGCTATTAAAC 739
Qy 662 AAAATATCTAAATATAGTAATCTATTTGGCAAAATCACTATAGAGAAGGACTAAATAAAC 721
Db 740 GTAAAAATACAAGATATACTGACTATGTATACAAACGTACAAATGAGGACTAACTATGA 799
Qy 722 TTGGAACGAACCTAATATGAGATGGAGTATATTTAATGATTTATCGAAGATATATGACTA 781
Db 800 TTAGAACTTAATACTAAACGAACATGGAATATGTATAATATCTTACCGTTTGAAGATGACTC 859
Qy 782 TTACTGTATTAGACTACTATCGCTCAATTTTCTTTTATGATATAAAGAGATACAAAGATT 841
Db 860 TAACTGTGTAGATCTTATGCTATTTTTCGAAATTAAGCCAGAAAATA----- 911
Qy 842 CAATAGGAAGAAATAGGTGGCATTTAAACCTGAACCTTAAGAGAAATTTATACAACTGAAA 901
Db 912 -----TCCAATAGGAGTTAAATCTGAACCTTACCAGAGAAGTTTATACGAATGTTA 961
Qy 902 TAAATTTTGACCGTCTTACTTACCTTGAATTTCAACCCCAATCTCGCTATAATGGAATATA 961
Db 962 -----ATTGAGTACATTTTGAACCAATTAACAGAACTAGAAA 997
Qy 962 ATTTAACAGTTTCAGGCTTAGATTAATTTTCATTTTATAGTGAATTAATTTTATATACAA 1021
Db 998 ATGGATTAACTAGAAATCTCATATTAATTTTCTGATTAACCAAGCGGCTTTTACACAA 1057
Qy 1022 AAAATGAAACGTCAGGGAATCGTTTAGTTGGTATTTGCGAATCGTAAATAGATCTACTTATG 1081
Db 1058 GAAATTCGAGACATCTTGTGCTCTATGATATTTTCTTTTACAGGTAACCCAGATGG 1117
Qy 1082 CTACGACAGGAACCTGAAATATATATGGAGAAGAACAGGTCACCCCAACAAACAACTT 1141
Db 1118 CTTTACACATATAATGATGATCGCAACATAATCTGGGGAGCGGTTTCATGACATATTA 1177
Qy 1142 TAAATACCACTTTCGAATCCTATAAAGTTTCAATTTGTAACCTGATAGACAACTCTCTACTT 1201
Db 1178 TTTCTCAAGACACATCCAAAGTATTTCTTTTATAGAAACAAACCTATTTGATAGGTCG 1237
Qy 1202 CCCCTTTTCTTAACATATCTTTACAAATTAATCAAAATGAACTTTATTTAAATAATTCAC 1261
Db 1238 AAATTTGTCAGACATAGAGAGTACTCAGATATAATATATGAAATGATATTTTTCGAATA 1297
Qy 1262 CTAGTAATAAATTAACATATTCAGCTGGGGGAATTTATCTAATGATAAAAAACAACTG 1321
Db 1298 GCAGTGAAGTATTTTCGATTTTTCATCAATTCACAAATAGAAAATTAATATAAAGAACTG 1357
Qy 1322 ATTTTCAATTTCTGTAAAAAAGACTGTAAACCAATTTAATCCAAATTTGTTTACCAA 1381
Db 1358 ATCTTTATATGATTTCCAAAACAAACATGGAAAAATTAAGAAATATGGTCATCTCTCGT 1417
Qy 1382 GCTATAAATAGTTATAGTCATATTTTATCCAGTTTCTTTTATTAATTAATTCCTATAAAA 1441
Db 1418 ATATAAAACTGATAATATATATTTTC----- 1445
Qy 1442 TTGGATTACCGCTAAATATATATATATACAGGTGGATAGGATGGACACAGTAGTGTTA 1501
Db 1446 -----AGTAGTTAGAGAAGAAGAAGAGTTGCAATTTAGTTGGACACATACTAGTTG 1498
Qy 1502 ATAGAAAATAGCAATATCAGATAAAATTAATTAATGATCCAGCAATCAAAAGGTAAACA 1561
Db 1499 ATTTCCAAAATACATAGATTTAGATATACATCCCAAAATCCACGCTCTAAAGCTTGA 1558

Qy 1562 GTCCTGATACAAACTCTAAGGTAAATTTGAAGNCCCTGGTTCATACAGAGGAAACTTGGTTT 1621
Db 1559 AGGTAAGTTCTGATTCGAAAATTTGGAAGGTCCTGGTTCACACAGGTGGAGACTTGGTAA 1618
Qy 1622 ATTTCAAAAGTCAAGGGCGTTTAGAGATTACATGTAGAACTCCTAATTTCCACACAATCTT 1681
Db 1619 TCTTAAAGATAGTATGATTTTAGAGTTAGATTTTAAANAATGTTTCTCCACAAT--- 1675
Qy 1682 ATTACATTAGACTTCGATACGCTACAAATGGTGGGAAATATCTTCTCTAATATATCTC 1741
Db 1676 ATCAAGTACGTATTCGTTATGCTACTAATGCTCCAAAGACACACAGTA--TTCTTAACCGG 1733
Qy 1742 TTACAATACCAGGAGTAAATAGGAATACCACCTCAAGGACTCAACACACTTTTCTCGGTA 1801
Db 1734 AATAGATACTATAAGTGTGGAGCTCCCTAGTACCACTTCCCGCCAAAAC-----C 1783
Qy 1802 CAATATAATAAATTTACAATACGAGATTTTGGGTATTTCCAAATTTCCAAGTACAGT-- 1859
Db 1784 CAATGCTACAGATTTAATCATATGCAATTTTGGATATGTAACATTTCCAAGAACAGTTC 1843
Qy 1860 -----AACATTACCTTTAAATCGAAACATACCACTTTATATTTAATCGTGCAAGATGAT 1912
Db 1844 CAATATAAACAATTTGAAGGAGAGACACTTTTATTAATGACCTTATATGTCACACAAATC 1903
Qy 1913 CAATTTCAATTTAATCATTTGATTAATAATTTGATTTTATACCAATTTCTCTCTGACGCC 1972
Db 1904 ATTCATATAATATATATATTTGACAAAATCGAATTTTATTTCCAAATCACTCAATCTGTATTAG 1963
Qy 1973 AAAATAGAGAAAAACAAAAATTTAGAAAATATCCTCAAAACAAAAATAAATATACATTTTTCACAA 2032
Db 1964 ATTATACAGAGAGCAAAATATAGAAAAACACAGAAAATAGTGAATGATTTATTGTTA 2023
Qy 2033 ATCATACAAAAAATACTTTTAAATATAGA 2060
Db 2024 ATTTAAACAAAGTTCCTTACTAAATAGA 2051

RESULT 14

AAAN50525
ID AAAN50525 standard; DNA; 3756 BP.
XX
AC AAAN50525;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 23-OCT-1991 (first entry)
XX
DE Bacillus thuringiensis var. israelensis endotoxin insert in plasmid
DE PSY367.
XX
KW Endotoxin; insecticide; ss.
XX
OS Bacillus thuringiensis serovar israelensis.
XX
PN EP153166-A.
XX
PD 28-AUG-1985.
XX
PF 15-FEB-1985; 85EP-00301017.
XX
PR 22-FEB-1984; 84US-00582506.
PR 22-JAN-1985; 85US-00693556.
XX
PA (SYTR) SYNTRO CORP.
XX
PI Walfield AM, Pollock TJ;
XX
DR WPI; 1985-211724/35.
XX
PT Polypeptide active against Diptera insects - prepd. from DNA sequence
PT coding for BTI endotoxin using bacterial host.
XX

PS Disclosure; Page 15a-e; 27pp; English.

XX The B. thuringiensis var. israelensis endotoxin insert in pSV367 is
CC expressed in a bacterial host. The protein produced has insecticidal
CC activity against dipteran insects. (Updated on 25-MAR-2003 to correct PA
CC field.) (Updated on 24-OCT-2003 to standardise OS field)

XX
SQ Sequence 3756 BP; 1379 A; 566 C; 659 G; 1150 T; 0 U; 2 Other;

Query Match 7.1%; Score 148.2; DB 1; Length 3756;
Best Local Similarity 48.3%; Pred. No. 1.3e-15;
Matches 1001; Conservative 0; Mismatches 893; Indels 177; Gaps 14;

QY 2 TGTGTCAGGGAATACACATATGGTGATATTCGAGCATTTTGGCTAGCTGATACAA 61
DB TGTGTCAGGGAATACACATATGGCAATATGGCAATATTCGAGCATTTTGGCTAGCTGATACAA 1148

QY 62 TTGCTGCAGTTAGTGCAAGTACTATTTGATCCGGTACTCTGTTAGCGGATAGGTGGGC 121
DB TTGCTGCAGTTAGTGCAAGTACTATTTGATCCGGTACTCTGTTAGCGGATAGGTGGGC 1208

QY 1149 TTGTTGGAGTTAGTGCAAGTACTATTTGATCCGGTACTCTGTTAGCGGATAGGTGGGC 181
DB TTGTTGGAGTTAGTGCAAGTACTATTTGATCCGGTACTCTGTTAGCGGATAGGTGGGC 1244

QY 122 TCACCTTCTATATCCGACCGATAGGAATAATAGGTGCTATTAATAATCTTTTGGTACCC 181
DB TCACCTTCTATATCCGACCGATAGGAATAATAGGTGCTATTAATAATCTTTTGGTACCC 1244

QY 182 TAATCACTGCTTTTGGCCCGGGAGAACACAGACAAACAGTATGACACAAATTTATTA 241
DB TAATCACTGCTTTTGGCCCGGGAGAACACAGACAAACAGTATGACACAAATTTATTA 1301

QY 1245 TGTGCGCATCTTTTGGCAAGGATCTGACCCG---CAAAATGTTTGGCAGGATTTGTTAA 301
DB TGTGCGCATCTTTTGGCAAGGATCTGACCCG---CAAAATGTTTGGCAGGATTTGTTAA 1358

QY 242 AAATGGAGAAATTTTGTGATACACCGTTTAAACAGAAACATTAACAGCTAAAGTTAC 361
DB AAATGGAGAAATTTTGTGATACACCGTTTAAACAGAAACATTAACAGCTAAAGTTAC 1415

QY 1302 ACATCGGAGGAGCGCTTATACAGAAATAGATTAACAAATTAATGATGTAACCT--- 1358
DB ACATCGGAGGAGCGCTTATACAGAAATAGATTAACAAATTAATGATGTAACCT--- 361

QY 302 AAACCTTTAGAGGATTTAGACAAATATTACAAAGCTATAATACAGCAATTAGATGGA 421
DB AAACCTTTAGAGGATTTAGACAAATATTACAAAGCTATAATACAGCAATTAGATGGA 1474

QY 362 GAAATTTAAAGACTCAAGCTCTGATTTACACCATCATCAGCAATTACACCAAGCTG 481
DB GAAATTTAAAGACTCAAGCTCTGATTTACACCATCATCAGCAATTACACCAAGCTG 1511

QY 1416 GGGAGCCAGCAGCTACACAGCTAATGCTAAGCAGTA-CATGATCTCTTTTACTACCTTA 541
DB GGGAGCCAGCAGCTACACAGCTAATGCTAAGCAGTA-CATGATCTCTTTTACTACCTTA 1565

QY 422 CCTGACTCTTAAATACGATTTGAGAAATGTTCAATGATTTTATTCGAGAAATACCTG 601
DB CCTGACTCTTAAATACGATTTGAGAAATGTTCAATGATTTTATTCGAGAAATACCTG 1625

QY 1475 GAACCTTAATAGATAAAGATTTAGATATGTTTAA--- 1511
DB GAACCTTAATAGATAAAGATTTAGATATGTTTAA--- 661

QY 482 GTTTTCAACCTTTGAAACCTTTTAAACCGCTATTACTACCTATTATTGCGCAAGCTGTAAT 541
DB GTTTTCAACCTTTGAAACCTTTTAAACCGCTATTACTACCTATTATTGCGCAAGCTGTAAT 1565

QY 1512 -----ATAATGCTAGCTATCGATACCAACACTCCCTGCTATATGCACAAATAGCTACTT 601
DB -----ATAATGCTAGCTATCGATACCAACACTCCCTGCTATATGCACAAATAGCTACTT 1625

QY 542 TTCAATTTAAATTTTAAACAAAGGCTGTAATTTGGCTGATGAATGGAATGCAGATATAC 661
DB TTCAATTTAAATTTTAAACAAAGGCTGTAATTTGGCTGATGAATGGAATGCAGATATAC 1679

QY 1566 GGCACCTTGAATTTTAAACAAAGGCTGTAATTTGGCTGATGAATGGAATGCAGATATAC 721
DB GGCACCTTGAATTTTAAACAAAGGCTGTAATTTGGCTGATGAATGGAATGCAGATATAC 1739

QY 602 ATCCTTCAAAATTTGAACTTAATGCTGGAACATCAGATGACTATTATAAACTTTTAAAG 781
DB ATCCTTCAAAATTTGAACTTAATGCTGGAACATCAGATGACTATTATAAACTTTTAAAG 1799

QY 1626 GT-----ATAATTCAGGACTTTTCAATTCATCTAATTTACTATCAGGGCTATTTTAAAC 841
DB GT-----ATAATTCAGGACTTTTCAATTCATCTAATTTACTATCAGGGCTATTTTAAAC 1851

QY 662 AAAATATACCTTAAATATAGTAACCTATTGTCGAAATACCTATAGAGAGGACTAAATAAAC 901
DB AAAATATACCTTAAATATAGTAACCTATTGTCGAAATACCTATAGAGAGGACTAAATAAAC 1901

QY 1680 GTAAATATACAGATATATCTGACTATTGTAACAAAGCTACAAATGAGGACTAATGTA 781
DB GTAAATATACAGATATATCTGACTATTGTAACAAAGCTACAAATGAGGACTAATGTA 1901

QY 722 TTCGAAAGCAACCTTAAATATAGAGTGGAGTATTTAATGATTTATGGAATATATGACTA 1799
DB TTCGAAAGCAACCTTAAATATAGAGTGGAGTATTTAATGATTTATGGAATATATGACTA 841

QY 1740 TTAGAACTTAACTAAACGCAATGGAATATGTAATATCTTACCTTTAGAAATGACTC 841
DB TTAGAACTTAACTAAACGCAATGGAATATGTAATATCTTACCTTTAGAAATGACTC 1851

QY 782 TTACTGTAATAGTACTATCTCCTCAATTTTCTTTTATGATATAAAGATACAAAGATT 901
DB TTACTGTAATAGTACTATCTCCTCAATTTTCTTTTATGATATAAAGATACAAAGATT 1901

QY 1800 TAACTGTGTTAGATCTTATGCTATTTTCCAAATTTATGACCCGAGAAATA----- 1851
DB TAACTGTGTTAGATCTTATGCTATTTTCCAAATTTATGACCCGAGAAATA----- 901

QY 842 CAATAGGAAGAAATAGGTGGCACTTAAACCTGAACTTTACAGAGAAATTTATACAACTGAAA 1901
DB CAATAGGAAGAAATAGGTGGCACTTAAACCTGAACTTTACAGAGAAATTTATACAACTGAAA 2029

QY 902 TAAATTTTGACCGTCTTACTTACCTTGAATAATCAACCCCAATCTCGCTATAATGGAATATA 961
DB -----ATTGATACATTTAGAACCATTAACAGAACTAGAAA 1937

QY 962 ATTTAACAGCTTCAGGGCTTAGATTTATTTTTCATTTTATGATGATTTTTCATTTTATACAA 1021
DB ATTTAACAGCTTCAGGGCTTAGATTTATTTTTCATTTTATGATGATTTTTCATTTTATACAA 1997

QY 1938 ATGGATTAACTAGAAATCTTACATTTTACTTTGGATTAACCAAGGGCGTTTATACAA 1081
DB ATGGATTAACTAGAAATCTTACATTTTACTTTGGATTAACCAAGGGCGTTTATACAA 2057

QY 1022 AAAATGAAACGTACGGGAATCGTTTGTGTTGTTTTCGGAATCGTAATAGATCTACTTATG 1141
DB AAAATGAAACGTACGGGAATCGTTTGTGTTGTTTTCGGAATCGTAATAGATCTACTTATG 2117

QY 1998 GAAATTTCTCGAGACATCTTGTATCTTATGATATTTTTCATTTTACAGGTAAACAGATGG 1201
DB GAAATTTCTCGAGACATCTTGTATCTTATGATATTTTTCATTTTACAGGTAAACAGATGG 2177

QY 1082 CTACGACAGAACTGAAATTTATATATGAGGAGAAAGACAGCTCCACCCACAAACAACTT 1261
DB CTACGACAGAACTGAAATTTATATATGAGGAGAAAGACAGCTCCACCCACAAACAACTT 2237

QY 2058 CTTTTACACATCTAATGATGATCGCAACATATCTGGGAGCGGTTTCATGGAATATTA 1321
DB CTTTTACACATCTAATGATGATCGCAACATATCTGGGAGCGGTTTCATGGAATATTA 2297

QY 1142 TAATACATTTGATCTTAAAGTTTCAATTTGTAATCTGATAGACAGTAACCTCTACTT 1381
DB TAATACATTTGATCTTAAAGTTTCAATTTGTAATCTGATAGACAGTAACCTCTACTT 2357

QY 2118 TTTCTCAAGACACATCCAAAGTATTTTCTTTTATAGAAACAACTTATTTGTAAGGTG 1441
DB TTTCTCAAGACACATCCAAAGTATTTTCTTTTATAGAAACAACTTATTTGTAAGGTG 2385

QY 1202 CCGCTTTTCTTACATATATCTTTTACAAATTAATCAAACTTTTATTTTAAATTAATTCAC 1501
DB CCGCTTTTCTTACATATATCTTTTACAAATTAATCAAACTTTTATTTTAAATTAATTCAC 2438

QY 2178 AAATGTCAGACATAGAGGACTCTAGATATATATGAAATGATATTTTTCGGAATA 1561
DB AAATGTCAGACATAGAGGACTCTAGATATATATGAAATGATATTTTTCGGAATA 2498

QY 1262 CTAGTAAATTAATTAACATATTCAGCTGGGGGAAATTTATCTAATGATAAATAAACAACCTG 1621
DB CTAGTAAATTAATTAACATATTCAGCTGGGGGAAATTTATCTAATGATAAATAAACAACCTG 2558

QY 2238 GCACTGAAGTATTTTCGATATTCATCAATTTCAACAATAGAAAATAATTTATATAAAGAACTG 1681
DB GCACTGAAGTATTTTCGATATTCATCAATTTCAACAATAGAAAATAATTTATATAAAGAACTG 2615

QY 1322 ATTTTCAATTTCTGTAATAAAGACTGTAAACCAATTTATTAATCCAAATTTGTTTACCA 1741
DB ATTTTCAATTTCTGTAATAAAGACTGTAAACCAATTTATTAATCCAAATTTGTTTACCA 2673

QY 2298 ATTTCTTATGATTTTCAAAACCAACATGGAATAATGAAGAAATATGTCATCTACTT 1801
DB ATTTCTTATGATTTTCAAAACCAACATGGAATAATGAAGAAATATGTCATCTACTT 2723

QY 1382 GCTATATAGTTATGATCTATTTTATCCAGTTTCTTCTTTTATTTTAAATTAATTCATATA 1859
DB GCTATATAGTTATGATCTATTTTATCCAGTTTCTTCTTTTATTTTAAATTAATTCATATA 2783

QY 2358 ATATAAAACGTAAATTAATTAATTTTCT----- 2385
DB ATATAAAACGTAAATTAATTAATTTTCT----- 1909

QY 1442 TTGGATTTAGCGCTTAAAT 2843
DB TTGGATTTAGCGCTTAAAT 1969

QY 2386 -----AGTAGTTAGAGAAAGAAAGAGTTCGATTTAGTTGGACACATCTAGTCTG 2903
DB -----AGTAGTTAGAGAAAGAAAGAGTTCGATTTAGTTGGACACATCTAGTCTG 2029

QY 1502 ATAGAAATTAATGCAATATCAGATAAATAATTAATTAATGATCCAGCAATCAAGGTAAACA 1621
DB ATAGAAATTAATGCAATATCAGATAAATAATTAATTAATGATCCAGCAATCAAGGTAAACA 2498

QY 2439 ATTTCCAAATATACAAATAGATTTAGATAAATCAACCCAAATCCACGCTCTTAAAAACTTTAA 1621
DB ATTTCCAAATATACAAATAGATTTAGATAAATCAACCCAAATCCACGCTCTTAAAAACTTTAA 2558

QY 1562 GTCTGTATACAACTCTTAAGTAATTCAGAGGCTGCTCATACAGAGGAAACCTTTGGTTT 1681
DB GTCTGTATACAACTCTTAAGTAATTCAGAGGCTGCTCATACAGAGGAAACCTTTGGTTT 2615

QY 2499 AGTTAAGTCTTAATTTCAAAATTTGTGAAAGGCTCGGTGACAAAGTGAAGAACTTTGGTAA 1741
DB AGTTAAGTCTTAATTTCAAAATTTGTGAAAGGCTCGGTGACAAAGTGAAGAACTTTGGTAA 2673

QY 1622 ATTTACAAAGTCAAGGCGTTTATAGAGATTACATGTAGAACTCTTAAATTTCTACAACTTT 1801
DB ATTTACAAAGTCAAGGCGTTTATAGAGATTACATGTAGAACTCTTAAATTTCTACAACTTT 2723

QY 2559 TTCTTAAAGATAGTATGAAATTTTAGAGTTAGATTTTAAATAATGTTTCTCAACAA---T 1859
DB TTCTTAAAGATAGTATGAAATTTTAGAGTTAGATTTTAAATAATGTTTCTCAACAA---T 2783

QY 1682 ATTTACATTTAGACTTCGATACGCTACAAATGGTGTGGAATATCTTCTTAAATATATCTC 1909
DB ATTTACATTTAGACTTCGATACGCTACAAATGGTGTGGAATATCTTCTTAAATATATCTC 2843

QY 2616 ATCAAGTACGCTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1969
DB ATCAAGTACGCTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2903

QY 1742 TTACAAATACAGGAGTAATAGGAATACCACTCAACGACTCAACAACTTTTCTCTGTTA 2029
DB TTACAAATACAGGAGTAATAGGAATACCACTCAACGACTCAACAACTTTTCTCTGTTA 2029

QY 2674 AATAGTACTATAGTCTGGAGCTCCCTAGTACCACTTCGCGCCAAAC-----C 2723
DB AATAGTACTATAGTCTGGAGCTCCCTAGTACCACTTCGCGCCAAAC-----C 2723

QY 1802 CAAATTAATAATTAATTAACAATACGAGATTTTGGGATTTTCCAAATTTTCCAAAGTACAGT-- 1859
DB CAAATTAATAATTAATTAACAATACGAGATTTTGGGATTTTCCAAATTTTCCAAAGTACAGT-- 2783

QY 2724 CAAATGCTACAGATTTTAAACATATGACAGATTTTGGATATGTAACATTTTCAAGAAACAGTTT 1909
DB CAAATGCTACAGATTTTAAACATATGACAGATTTTGGATATGTAACATTTTCAAGAAACAGTTT 2843

QY 1860 --AACATTTACCTTTAAATCGAAACATACCATTTATA-----TTTAAATCGTCAGATG 1969
DB --AACATTTACCTTTAAATCGAAACATACCATTTATA-----TTTAAATCGTCAGATG 2903

QY 2784 CAAATAAAACATTTGAAGGAGAGACACACTTTTATTAATGACCTTTTATTTATGTTGTTACACAA 2029
DB CAAATAAAACATTTGAAGGAGAGACACACTTTTATTAATGACCTTTTATTTATGTTGTTACACAA 2029

QY 1910 TATCAAAATTTCAATTTTAAATCAATTTGATTAATTTTATACCAATTTTCTCTCTGTTAC 2029
DB TATCAAAATTTCAATTTTAAATCAATTTGATTAATTTTATACCAATTTTCTCTCTGTTAC 2029

QY 2844 ATCAATTCATTAATTAATTAATTTGACAAATTTGAAATTTTATTTTCAATCTCAATCTGTTAT 2029
DB ATCAATTCATTAATTAATTAATTTGACAAATTTGAAATTTTATTTTCAATCTCAATCTGTTAT 2029

QY 1970 GCCAAATAGAGAAAAACAAAAATAGAAACTATCCCAACAAAAATAAATACATTTTTCAT 2029
DB GCCAAATAGAGAAAAACAAAAATAGAAACTATCCCAACAAAAATAAATACATTTTTCAT 2029

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Db      2904 TAGATTATACAGAAAGCAAAATATAGAAAAACACAGAAATAGTGAATGATTTATTG 2963
QY      2030 CAAATCATACAAAAATACTTTTAAATATAGA 2060
Db      2964 TTAAATTAACAAGTCTTACTAATAATAGA 2994

RESULT 15
ID      ABL34155/c
XX      ABL34155 standard; DNA; 15548 BP.
XX      ABL34155;
XX      26-MAR-2002 (first entry)
XX      Human immune system associated gene SEQ ID NO: 2128.
XX      Human; immune system disease; cytosine methylation; antiasthmatic;
KW      antarteriosclerotic; anti-naemic; cytosine; cytosine; cytosine; cytosine;
KW      neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW      antineuritic; antidiabetic; antipsoriatic;
KW      antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW      acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW      neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW      ds.
XX      Homo sapiens.
OS      OS
XX      WO200200928-A2.
XX      03-JAN-2002.
XX      02-JUL-2001; 2001WO-EP007537.
XX      30-JUN-2000; 2000DE-01032529.
XX      01-SEP-2000; 2000DE-01043826.
XX      (EPIG-) EPIGENOMICS AG.
XX      Olek A, Piepenbrock C, Berlin K;
XX      WPI; 2002-130909/17.
XX      Nucleic acid comprising fragment of chemically modified gene, useful for
PT      diagnosis and treatment of diseases associated with abnormal cytosine
PT      methylation.
XX      Claim 1; SEQ ID NO 2128; 32pp + Sequence Listing; German.
XX      The present invention provides a number of human immune system associated
CC      genes which are modified by the methylation of cytosines. The sequences
CC      can be used in the diagnosis and treatment of immune system disorders,
CC      including eye diseases such as retinopathy, neovascular glaucoma and
CC      macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC      leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC      rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC      diseases. The present sequence is a gene of the invention
XX      Sequence 15548 BP; 4209 A; 247 C; 2903 G; 8189 T; 0 U; 0 Other;
SQ      Query Match 5.6%; Score 117; DB 6; Length 15548;
      Best Local Similarity 43.6%; Pred. No. 2.1e-10;
      Matches 819; Conservative 0; Mismatches 1040; Indels 18; Gaps 6;
QY      218 AACGCTATGGACACATTTTAAATCGGAGAAATTTTGTGATACACCGTTAACAG 277
Db      13398 ATAAATATACACGCATAAAATATATACGTATATAAAATATATATATAAAATATACACGT 13339
QY      278 AAAGCTATAAACGCTAAAGTTTACAACTTTTGAAGGATTTAGACAAATATTACAAAGCT 337
Db      13338 CTAAATATATATATAAAATATTCCCGTATAAAATATATATCTCTAAATATATATATAT 13279

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QY      338 ATAATACAGCATTAGATGATTTGGAGAAATTTAAAGACTACAAGCTCCTGGATTACCAC 397
Db      13278 AAAATATATATCTAAATATATATATAAAATATATATCTAAATATATATATAATAATA 13219
QY      398 CATCATCAGCATTTACAACAAGCTGCTTGCATCTCTAAATATAGGATTTGAGAAATGTTTCA 457
Db      13218 TATATCTAAATATATATATAAAATATATATCTAAATATATATATAAAATATATATATC 13159
QY      458 ATGATTTTATTCGAGAAATACCTGTTTCCAACTTTGAAACTTATATAAAACGCTATTACTAC 517
Db      13158 TAAATATATATATAAAATATATATCTAAATATATATATAAAATATATATAATA 13099
QY      518 CTATTTATGCGCAAGCTGCTAAATTTTCAATTTTAAATTTTATTAACAACAGGTGCTGAATTGG 577
Db      13098 ATATATATATATAA--AATATATAAAATATATATATAAAATATATATAATAATA 13042
QY      578 CTGATGAATGGAATGCAGATACATACCTTTCACAAATTCGAACCTAATGCTGGAACATCAG 637
Db      13041 TACATATATAAAATATATATATACAATATACATATATAAAATATACATATATACAATAT-AT 12983
QY      638 ATGACTATTATAAACTTTTAAAGAAATATACCTAAATATATAGTAACTATTGTGCAATA 697
Db      12982 ATATAAAATATATATAAAATATATATAAAATATATATAAAATATATATAACGAAATA 12923
QY      698 CCTATAGAGAGGACTAAATAACTTCGAAACGAACCTAAATATGAGATCGAGTATATTTA 757
Db      12922 TATATATACGAAATATATATAAATATATATATACGAAATATATATACGAAATATATATA 12863
QY      758 ATGATTATCGAAGATATATGACTATTCTGTATTAGATCTACTCGCTCAATTTTCTTTTT 817
Db      12862 TAAATATATACGAAATATATATATACGAAATATATATATAAATATATATAATATATAT 12803
QY      818 ATGATATAAAGAGATACAAAGATTCATAGAGAAATAGGTGCGCATTAATAAACTGAACTTA 877
Db      12802 ACGAAATATATATACGAAATATATATAAATATATATAAATATATATAAATATATATACGAAA 12743
QY      878 CAAGAGAAATTTATACAACTGAAATAAATTTTGCAGCTCTTACTTACCTTGAAATTCAC 937
Db      12742 TATATATATAATATATATAAATATATATATA-CGAAATATATATAAATATATATATAT 12684
QY      938 CCAATCTCGCTATAAATGGAATATAATTTAAACAGTTTCAGGCTTAGATTATTTTCAATTT 997
Db      12683 AAAATATATATACGAAATATAATATAATATATATAAATATATATAAATATATATACGAAATA 12624
QY      998 TAGATGAAT-TATATTTTATACAAAAATGAAACGTACGGGAATCGTTTAGTTGTTAT 1056
Db      12623 TATATAAATATATATATAAATATATATAAATATATATAAATATATATAAATATATATACA 12564
QY      1057 GCGAATCGTAATAGATCTACTTATGCTACGACAGGAACCTGAAATATATATATGAGAAAGA 1116
Db      12563 TAAATATATATATAAATATAAATATATACATAAATATATATAAATATATAAATATATACATA 12504
QY      1117 ACAGGTCCACCCACACAAAAACTTTA-----ATACCAATTTGAAATCCTATAAAGTT 1167
Db      12503 ATATATATATAAATATATACATAAATATATATAAATATATAAATATATATAAATATAT 12444
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Db      12443 ATATATAAACAATATATACATAAATATATATAAATATATAAATATATATAAATATATATAT 12384
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Db      12383 ATATAACATATATATATAAATATATAAATATATAAATATATAAATATATAAATATATATAT 12324
QY      1288 GGGGGGAAATTTATCTAAATGATAAAAAACAACCTGATTTTCAATTTTCTCTGTAATAAAGAC 1347
Db      12323 AACATATATATATAAACAATATATAAACAATATATAAACAATATATAAACAATATATAAACA 12264
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Db      12263 TATATATATAAACAATATATAAACAATATATAAACAATATATAAACAATATATAAACAATATA 12204
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 00:17:12 ; Search time 8388 Seconds
(without alignments)
11629.836 Million cell updates/sec

Title: US-10-782-570-3
Perfect score: 2085
Sequence: 1 atgtgtcaagggaatacaca.....caaacatgatattgattaa 2085

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hic.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gss1.*
10: gb_gss2.*
11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	100	4.8	2157	10	CL081966
C 2	98.4	4.7	1758	10	CL509408
C 3	95.2	4.6	1981	10	CL082000
C 4	90.2	4.3	1392	10	CG757503
C 5	90	4.3	1539	10	AG340947
C 6	90	4.3	1896	10	CG753083
C 7	89.4	4.3	1542	10	AG386981
C 8	88.8	4.3	1608	10	CL118721
C 9	88.4	4.2	1489	10	AG350139
C 10	87.2	4.2	734	10	CNS010MP
C 11	86.8	4.2	1348	10	CG749499
C 12	86	4.1	1101	10	CNS00EVL
C 13	85	4.1	1391	10	CG754863
C 14	84.6	4.1	1242	10	CL068807
C 15	84.6	4.1	2270	10	AG279272
C 16	81.4	3.9	994	11	CNS04NOJ
C 17	81	3.9	1272	1	AJ927522
C 18	80.6	3.9	1271	10	CG748753
C 19	79.8	3.8	1038	11	CNS06L7M
C 20	79.8	3.8	1101	10	CNS0039G
C 21	79.8	3.8	1238	1	AJ925855
C 22	79.4	3.8	1254	10	AG349719

C 23	79.2	3.8	1928	10	CL073845
C 24	78.8	3.8	1594	10	CL110653
C 25	78.6	3.8	1592	10	CG750135
C 26	78.2	3.8	1592	10	CG750135
C 27	78.2	3.8	1605	8	DN712410
C 28	78.2	3.8	1811	10	CG753732
C 29	77.6	3.7	1632	10	CL082569
C 30	77.4	3.7	1095	1	AJ926415
C 31	77.4	3.7	1313	7	CK997149
C 32	77.4	3.7	1388	10	AG278124
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C 34	76.4	3.7	1200	1	AJ928743
C 35	76.4	3.7	1277	9	CC353231
C 36	76.4	3.7	1380	1	AJ928744
C 37	76.4	3.7	1626	6	CF238805
C 38	76.4	3.7	1807	10	AG333676
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C 40	76.2	3.7	1210	10	CG749728
C 41	76.2	3.7	1272	9	CC264939
C 42	76.2	3.7	1896	10	CG753083
C 43	76	3.6	1962	10	AG390999
C 44	75.8	3.6	1101	10	CNS0039G
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ALIGNMENTS

RESULT 1
CL081966/c
LOCUS
DEFINITION
CH216-165D13 Sp5.1 CH216 Xenopus tropicalis genomic clone
CH216-165D13, genomic survey sequence.
ACCESSION
CL081966
VERSION
GSS.
KEYWORDS
CL081966.1 GI:40537879
SOURCE
Xenopus tropicalis (western clawed frog)
ORGANISM
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE
1 (bases 1 to 2157)
Kremtzki,C., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.
AUTHORS
A physical map of the xenopus tropicalis genome
TITLE
Unpublished (2003)
JOURNAL
Contact: Richard K Wilson
COMMENT
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
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Class: BAC ends
High quality sequence start: 341
High quality sequence stop: 412.
Location/Qualifiers
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/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis BAC library"

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Best Local Similarity 43.6%; Pred. No. 2.5e-08;
Matches 645; Conservative 0; Mismatches 820; Indels 13; Gaps 4;

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DB 1715 AATCAAAATATATATATATACAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1661
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DB 1660 AAAAAAATAAATACAAAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1601
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QY 1028 AAGCTGACGGGAATCGTTTGTGTTGTTGCGAATCGTAATAGATCTACTTATGTCACGA 1087
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DB 1001 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 942
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QY 1568 ATACAAATCTAAGGTAAATTTGAAGGACCTGGTTCATACAGAGGAACTTGGTTTATTTAC 1627
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QY 1628 AAGTCAAGGCGCTTTAGAGATTACATGATAGAACTCCTAATTTCTACACAACTTTATACA 1687
DB 767 TTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 708
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DB 707 AAAAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 648
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DB 647 AATATATTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 588
QY 1808 ATAAATAATTTCAATACGAGATTTTGGGTATTTTCCAAATTTCCAAATTCAGTACATTAC 1867
DB 587 ATAAATAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 528
QY 1868 CTTTAAATCGAAACATACCATTATATTTAATCGTGACATGTATCAAAATTTCAATTTAA 1927
DB 527 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 468
QY 1928 TCATTGATAAATAATGAATTTTATACCAATTTACTTCTCTGTAGCCCAAAATAGAGAAAAC 1987
DB 467 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 408
QY 1988 AAAAAATTGAAACTATCCAAACAAAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2047
DB 407 AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 348
QY 2048 CTTTAAATATAGAGCCCAAACTATGATATTGATTAA 2085
DB 347 AAAAAAACCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 310

RESULT 2
LOCUS CL509408
DEFINITION SAIL_811_H11.v3 SAIL Collection Arabidopsis thaliana genomic clone
ACCESSION CL509408
VERSION CL509408.1 GI:46006728
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1758)
AUTHORS Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
TITLE A high-throughput Arabidopsis reverse genetics system
JOURNAL Plant Cell 14 (12), 2985-2994 (2002)
PUBMED 12468722
COMMENT Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number CS836276; T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: TDNA tagged.
FEATURES
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/note="T-DNA left border sequences were isolated using a
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ORIGIN
Query Match 4.7%; Score 98.4; DB 10; Length 1758;
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[illegible]

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Matches 620; Conservative		0; Mismatches 798; Indels 16; Gaps 3;	
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QY	718	AACTTCGAAACCACTTAATAGATGGAGTATATTTAATCATTTATCGAAGATATAG	777
DB	1918	AAAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1859
QY	778	ACTATTACTGTATTAGATACATTCGCTCAATTTTCTTTTAA-----TGATATAA	826
DB	1858	TAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1799
QY	827	AGAGATACAAAGATTCAATAGGAAGATAGGTGGCAATTTAAACTGAACCTTACAGGAA	886
DB	1798	ATATATAAAAAATAAATAACACAAAAAATAAATAAATAAATAAATAAATAAATAA	1739
QY	887	TTTATACAACTGAATAAATTTTGACGCTCTTACTTTACCTTGAATTCACCCCAATCTG	946
DB	1738	TAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1679
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DB	1678	AAAAATCTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1619
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DB	1558	AAATAATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1499
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DB	1018	AAAAAAAAATACATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	959
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DB	958	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	899
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DB	898	ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	841
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DB	840	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	781
QY	1844	AATTTCAAGTACAGTAAACATTACCTTTTAAATCGAAACATACATTTATTTAATCGTG	1903
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QY	1904	CAGATGTATCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTT	1963
DB	720	ATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	661
QY	1964	CTGTACGCCAAATATAGAGAAAAACAAATTTAGAAATCTCCAAACAAAAATAAATACAT	2023
DB	660	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	601
QY	2024	TTTTCAAAATCATACAAAAATATCTTTAAATATAGAGCCCAAACTATGATA	2077
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LOCUS			
DEFINITION			
P052-4-C08.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,			
genomic survey sequence.			
ACCESSION			
CG757503			
VERSION			
CG757503.1 GI:37986131			
KEYWORDS			
GSS.			
SOURCE			
Pristionchus pacificus			
ORGANISM			
Pristionchus pacificus			
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;			
Neodiplogasteridae; Pristionchus.			
REFERENCE			
1 (bases 1 to 1392)			
AUTHORS			
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,			
Buntjer,J., van der Meulen,M. and Sommer,R.J.			
TITLE			
An integrated physical and genetic map of the nematode Pristionchus			
JOURNAL			
Mol. Genet. Genomics 269 (5), 715-722 (2003)			
PUBMED			
12884007			
COMMENT			
Contact: Sommer RJ			
Evolutionary Biology			
Max-Planck-Institute for Developmental Biology			
Spemannstr. 37-39, Tuebingen D-72076, Germany			
Tel: 00497071601371			
Fax: 00497071601498			
Email: ralf.sommer@tuebingen.mpg.de			
Class: BAC ends.			
FEATURES			
Location/Qualifiers			
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Best Local Similarity			
Matches 412; Conservative			
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44.0%; Pred. No. 1.6e-06;			
0; Mismatches 523; Indels 1; Gaps 1;			

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1339 ATAAATAAAATTAATAAAATATTTAAATAATATATATATAAAATAAAATAAATA 1280
Qy 698 CCTATAGAGAGGACTAAATAAACTTCGAACGACCTAATATGAGATGAGTATATTTA 757
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1279 TAAATAAANAANAATAATTTATATAATAAATAAATAAATAAATAAATAAATAAATA 1220
Qy 758 ATGATTATCGAAGATATATGACTATTACTGTATTAGATACCTATCGCTCAATTTCTTTT 817
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1219 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1161
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1160 TATATTAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1101
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860 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 801
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800 TAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 741
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Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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LOCUS Mus musculus molossinus DNA, clone:MSMg01-134C16.T7, genomic survey
DEFINITION sequence.
ACCESSION AG340947
VERSION AG340947.1 GI:47914257
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KEYWORDS

SOURCE
ORGANISM

Mus musculus molossinus (Japanese wild mouse)
Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Mus;

REFERENCE

AUTHORS

1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,
Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriawaki, K. and
Shiroishi, T.
Contribution of Asian mouse subspecies *Mus musculus molossinus* to
genomic constitution of strain C57BL/6J, as defined by BAC-end
sequence-SNP analysis
Genome Res. 14 (12), 2439-2447 (2004)
15574823

REFERENCE

AUTHORS

2 (bases 1 to 1539)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail: hattori@gsc.riken.jp URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

COMMENT

Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@c.riken.jp).
Tei: 81-45-503-9111, Fax: 81-45-503-9170
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Tsukuba Institute, Bio Resource Center,
Tsukuba, Ibaraki, 305-0074 Japan
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@c.riken.jp

PRIMERS

Sequencing : T7

LIBRARY

Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.

FEATURES

source

1. 1539
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Db 151 ANNNNNNNNTNNNNNNNNNGGGGNAANAAGNTTTTAAAGCGNNC 102

CG753083 1896 bp DNA linear GSS 24-OCT-2003
P048-1-C01.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.
CG753083
CG753083.1 GI:37977199
GSS.
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1896)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)
12884007
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

Location/Qualifiers
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Matches 631; Conservative 0; Mismatches 858; Indels 12; Gaps 4;

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Db 1581 TATAAATAATTTATATATATTTTATATATTTTATATTTTATTAATAATAATAATAAT 1522
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[illegible]

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DEFINITION	ISB1-72J8_T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-72J8,		
ACCESSION	Genomic survey sequence.		
VERSION	CL118721		
KEYWORDS	CL118721.1 GI:40612356		
SOURCE	GSS.		
ORGANISM	Xenopus tropicalis (western clawed frog)		
	Xenopus tropicalis		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;		
REFERENCE	Xenopodinae; Xenopus; Silurana.		
AUTHORS	1 (bases 1 to 1608)		
	Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,		
	Mardis, E. and Wilson, R.		
TITLE	A physical map of the xenopus tropicalis genome		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Richard K Wilson		
	Genome Sequencing Center		
	Washington University School of Medicine		
	Email: submissions@watson.wustl.edu		
	Insert Length: 75000 Std Error: 0.00		
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Qy	755	TTAATGATTATCGAAGATATATGACTATTACTGTATTAGTACTATCGCTCAATTTTCTT	814
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Qy 1554 AGGTACAGCTTTGATACAACTCTAAGGTAAATTTGAAGGACCTGGTCATACAGGAGAA 1613

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Db 244 ATATAAATAATTTTATTTTAAATTTTAAATAAATAATTTTATATATAAATTTTATATATAAT 185

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Qy 2033 ATCATACAAAAAAT 2046

Db 124 GTCACACATATTT 111

CNS010MP 734 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN04120 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION AL099163
VERSION AL099163.1 GI:5610774
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 734)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11.

FEATURES
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Best Local Similarity 34.9%; Pred. No. 5.9e-06;
Matches 248; Conservative 111; Mismatches 341; Indels 10; Gaps 1;
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Db 9 TACANTACTCAWATATNMWMACTAAAAATTTATAAAAAAATAAATAATATATATATTA 68

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RESULT 15

AG279272/c

LOCUS

DEFINITION

sequence.

ACCESSION

AG279272

VERSION

AG279272.1

GI:47852149

KEYWORDS

GSS.

SOURCE

Mus musculus molossinus (Japanese wild mouse)

ORGANISM

Mus musculus molossinus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Mori, K., and Shiroishi, T.

Contribution of Asian mouse subspecies *Mus musculus molossinus* to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis

Genome Res. 14 (12), 2439-2447 (2004)

15574823

2 (bases 1 to 2270)

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Direct Submission

Submitted (17-NOV-2003) Masahito Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan

(E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the mouse BAC library MSG01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

Taukuba Institute Bio Resource Center.

The Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

Phone: 81-298-36-9189, Fax: 81-298-36-9199

e-mail: abe@rtc.riken.jp

PRIMERS

Sequencing : TJ

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI.

R.Site 2 : EcoRI.

Location/Qualifiers

1. : 2270

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/sub_type="genomic DNA"

/sub_species="molossinus"

/db_xref="taxon:57486"

/clone="MSG01-050A24.TJ"

/sex="male"

/tissue type="mixture of kidney and spleen"

/clone_lib="MSG01 Mouse Male BAC Library"

FEATURES

source

Query Match 4.1%; Score 84.6; DB 10; Length 2270;

Best Local Similarity 42.7%; Pred. No. 1.8e-05;

Matches 650; Conservative 0; Mismatches 869; Indels 5; Gaps 4;

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Qy 609 ACAAAATTGAACCTAATTCCTGGAAACATCAGATGACATTTATAAACTTTTAAAAAGAAATAT 668

Db 1911 ATAAAAAAGTAACTAATAAGAAAAAGAAAAAATAAATAAATAAATAAATAAATAAATAA 1852

Qy 669 ACCTAAATATAGTAATTTGTGCAAAATACCTATAGAGAAGACTAAATAAACTTCGAA 728

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Qy 789 ATTAGATATCTACGCTCAATTTTCTTTTATGATATAAAGAGATACAAAGATTTCAATAGG 848

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833 CAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 774
Qy 1746 AATACCAAGGAGTAATAGGAATACCACTCAACGACTCAACAACATTTTCTGGTACAA 1805
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Search completed: February 15, 2006, 02:57:59
Job time : 8397 secs

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RESULT 2

PCT-US94-07902-27

; Sequence 27, Application PC/TUS9407902

; GENERAL INFORMATION:

; APPLICANT:

; APPLICANT: Street address: 4980 Carroll Canyon Road

; APPLICANT: City: San Diego

; APPLICANT: State/Province: California

; APPLICANT: Country: US

; APPLICANT: Postal code/Zip: 92121

; APPLICANT: Phone number: (619) 453-8030

; APPLICANT: Telex number: Fax number: . (619) 453-6991

; TITLE OF INVENTION: Materials and Methods for the Control of

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David R. Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/07902

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Saliwanchik, David R.

; REGISTRATION NUMBER: 31,794

; REFERENCE/DOCKET NUMBER: MA79

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3543 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 PCT-US94-07902-27

Query Match 15.98; Score 331.4; DB 6; Length 3543;

Best Local Similarity 53.8; Pred. No. 3.3e-56; Indels 38; Gaps 7;
 Matches 856; Conservative 0; Mismatches 697;

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Db	901	ACTGCTGTATTAGATCTTGTGGCACTCTTCTCAATTTATGATGATAGGTAATATCCAAATA	960
Qy	859	GGCAATTAACCTGAACCTTACAAGAGAATTTATACAACTGAAATAAATTTTGACCGCTTT	918
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Qy	919	ACTTACCTTGAATTTCAACCCAACTCTCGCTATATGGAATATAATTTAAACAGTTGAGG	978
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Qy	979	CTTAGATTATTTTCATTTTATGATGAACTTATATTTATACAAAATGAAACGTACGGG	1038
Db	1074	TTTATTTACTTTGGCTTGATTTCTTTGAATTTTATGAAAAGCGCAAACTCTCCTAATAA	1133
Qy	1039	AATCGTTTAGTTGGTATTCGAACTCGTAATAGATCTACTTT-ATGCTACGACAGGAACCTGA	1097
Db	1134	TTTTTTCACAGCCATTAATAATGTTTCATTACACTCTGATTAATATATCCAAAATC	1193
Qy	1098	AATTATATATGAGAAAGAACAGGTCCACCCACAAACAAATCTTTAATPACCAATTTGAATC	1157
Db	1194	TAGTGTTTTGGAAATCACAATGTAACGTATAAATTTAAATCTCTTGGTTGGCAACAAA	1253
Qy	1158	CTATAAAGTTTCAATTTGATGATAGACAGTAACCTCTACTCTCCCTTTTCCCTAAT	1217
Db	1254	TATTTATATTTTATTTAATATGTCATAAGCTTAGATAATAAATATCTAAATGATTATAA	1313
Qy	1218	ATACCTTTCAATTAATCAAAATGAACTTTATTTAAATAATTCACCTAGTAAATAATTAAC	1277
Db	1314	TAAATATAGTAAATGGATTTTATTAATCAATCGTACTAGACTTTGGAGAAAGAACT	1373
Qy	1278	ATATTTCAGCTGGGGGAAATTTATCTAATGATATAAAAAAACAACCTGATTTCAATTTCTGT	1337
Db	1374	TACACGAGGATCTGGGCAAAATAACTTATGATGATAAATAAATAATTTTCGGGTACCAAT	1433
Qy	1338	AAAAAAGACTGTAAACCAATTTAATCCAAATTTGTTTACCAGCTATATAGTTATAG	1397

Db	1434	TCCTAAACCAAGAGAGAGAAATCAAGCAATCCCTACCCCTTTTCCAAACATATGATAACTATAG	1493
Qy	1398	TCATATTTTATCCAGTTTCTTTTATTTAATTTATCTATAAATTTGGATTAGCGCTAAA	1457
Db	1494	TCATATTTTATCATTTTATTAATAAGTCTTAGTATCCC-----TGCACATATA	1538
Qy	1458	TATATTATATACAGGTGCAATTAGGATGGACACACAGTAGTGTGTTAATAGAAATATCAAT	1517
Db	1539	TAAACCTCAAGTGTATACGTTTCTGTTGGACACACTCTAGTGTGATCCTAAAAATACAAT	1598
Qy	1518	ATCAGATAAAATTAATTAATCAATGATCCAGCAATCAAAAGGTAAACAGTCTTGATCAAACTC	1577
Db	1599	TTATACACATTTAACTACCCAAATTCAGCTGTAAAAAGCGAATTCACCTGGGACTGCTTC	1658
Qy	1578	TAAGTAAATTAAGGACCTGCTCATACAGGAGGAACTCTGTTTATTATCAAAAGTCAAGG	1637
Db	1659	TAAGGTGTTTCAAGGACCTGGTATACAGGAGGGGATTTAATGATTTCAAGATCA---	1715
Qy	1638	GCCTTTAGAGATTACATGTAGAACTCTCTAATTTCTACAAATCTTTATTACATTAGACTTCG	1697
Db	1716	---TTTCAAAATTTACATGTCAACACACTCAAAATTTTCAACATCGTATTTTATAAGAAATCG	1772
Qy	1698	ATACGCTACAAATTTGGTCTCGAAATACTCTTCTTAATATATCTCTTACAAATPACCAGAGT	1757
Db	1773	TTATGCTTCAATTTGAAGCGCAAAATACACGAGCTGTATAAATCTTAGTATCCAGGGG-	1831
Qy	1758	AATAGGATACCACTCAACGACTCAACACACTTTTCTGTTGTTCAAAATATATAAATTT	1817
Db	1832	--TAGCAGAACTGGGTATGGCACTCAACCCCACTTTTCTGTTACAGATTATACGAATTT	1889
Qy	1818	ACAATACGAGATTTTGGGTATTTCCAAATTTCCAAATTTCCAAATTTACATTTACCTTTAAATTCG	1877
Db	1890	AAATATAAAGATTTTCAGTACTTAGAATTTTCTTAACGAGGTGAAATTTGCTCCAAATCA	1949
Qy	1878	AAACATACCAATTTATATTTAATCGTGAGATGAT---CAAATTCAAATTTTAATCATTTGA	1934
Db	1950	AAACATATCTCTGTGTTTAACTCGTTCGGATGTATATACAAACACACAGTACTTATTGA	2009
Qy	1935	TAAATTTGAATTTATACCAATTTACTCTCTGTACGCCAAATAGAGAAAAACAAAATTT	1994
Db	2010	TAAATTTGAATTTCTGCCAATTTACTCGTCTATAAGAGAGGATAGAGAGAAAAACAAAATTT	2069
Qy	1995	AGAACTATCAAAACAAAATAAATATACATTTTTCACAAATCATACAAAAATACCTTTAAA	2054
Db	2070	AGAAACAGTACAAATAATTAATATACATTTTATGCAATCTCTATAAATAAAACACTTTTACA	2129
Qy	2055	TATGAAGCCCAACAACTATGATTTGATTAA	2085
Db	2130	ATCAGAACTTACAGATTATGACATAGATCAA	2160

RESULT 3

US-09-224-024-30
 ; Sequence 30, Application US/09224024
 ; Patent No. 6056953
 ; GENERAL INFORMATION:
 ; APPLICANT: Leslie Hickle
 ; APPLICANT: Jewel Payne
 ; TITLE OF INVENTION: Materials and Methods for the Control of
 ; TITLE OF INVENTION: Calliphoridae Pests
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David R. Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: FL
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS


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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,024
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-224-024-30

Query Match      7.6%; Score 158; DB 3; Length 2061;
Best Local Similarity 48.3%; Pred. No. 4.3e-22;
Matches 999; Conservative 0; Mismatches 895; Indels 174; Gaps 13;

QY      2  TGTGTCGAAGGAATACACATATATGGTGATATTTTCGAGACATTTGCTAGTGTGATACAA 61
DB      149  TGTGTCGAAGTAATCAACATATATGGCAATATTCGGGGAAATTTGTAGTCTCGAACTA 208

QY      62  TTGCTGCAGTTAGTGCAGGTACTATTGTATPCGGTACTCTGTGTAGCGGATAGGTGGGC 121
DB      209  TTGTTGGAGTTAGTGCAGGTATTATTGTAGTAGGAACATGTTAGGAGCTTTTGTGCGCC 268

QY      122  TCACCTCTATATCCGGNCCGATAGGAATATAGGTGCTATATTAATATCTTTTGGTACCC 181
DB      269  -----CTGTCTTAGCTGCAGGTATATATCTTTTGGGACTT 304

QY      182  TAATCACTGTCTTTTGGCCCGGGAGAACACACAAACAGATATGACACAAATTTATTA 241
DB      305  TGTGTCGGATCTTTTGGCAAGGATCTGACCCCTG---CAATGTTTGGCAGGATTGTGTA 361

QY      242  AAATGGGAGAAATTTTGTGTATACACCGTTAAACAGAAAGCATATAACACAGCTTAAGTTAC 301
DB      362  ACATCGGAGGAGCCCTATACAGAAATAGATAAAACATAATTAATGTACTAACTT--- 418

QY      302  AAACCTTTAGAGGATTTAGACAATATATCAAAAGCTATATACAGCATTAGATGATGGA 361
DB      419  ---CTATCGTAACACCTATATAAAATCAACTTGTATAAATATCAAGAAATTTTTCGATAAAT 475

QY      362  GAAAAATTAAGACACTACAGCTCTCGGATTTACCAATCATCATCAGCATTACACAAAGCTG 421
DB      476  GAGAGCCAGCAGTACACAGCTTAATGCTTAAGCAGTA-CATGATCTCTTTACTACCTTA 534

QY      422  CCTTGTCTCTTAAATACGATTTGAGATGTTTCCAAATGATTTTATTCGAGAAATACCTG 481
DB      535  GAACCTATAATAGATAAAGATTTAGATATGTTAAAAA----- 571

QY      482  GTTTCCAACTTGAACCTTATAAACGCTTATTACTACTCTATTATGCGCAAGCTGTAAT 541
DB      572  -----ATAATGTAGCTATCGAATACCAACACTCCCTCGAATGACACAAATAGCTACT 625

QY      542  TTCATTTAAATTTATTACAAAGGTGCTGAAATTTGGCTGATGAATGAATTCAGATATAC 601
DB      626  GGCACCTTGAATTTATTAAACATGCTGCTACCTATTACATATATATGCTGCGCAAAATCAAG 685

QY      602  ATCCTTTCAAAATTTGAACCTTAATGCTGGAAACATCAGATGACTATTATAAATCTTTAAAG 661
DB      686  GT-----ATAAATCCAAGTACTTTCAATTCATCTAATTACTATCAGGGCTATTATAAAC 739

QY      662  ABAATATACCTAAATATAGTAATCTATTGTGCAATACCTATAGAGGAGGACTAAATAAAC 721
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DB      740  GTAAAAATCAAGAAATATCTGACTATTGTATACAAACGTACATGTCGAGGACTAAGTATGA 799
QY      722  TTCGAAACGAACCTAATATGAGATGGAGTATATTTAATGATTATCGAAGATATATGACTA 781
DB      800  TTAGAACTAATACTAACGCAACATGGAATATGTAATAATCTTACCCTTTAGAAATGACTC 859
QY      782  TTACTGTATTAGATACTACTCGCTCAATTTTCTTTTATGATATAAGAGATACAAAGATT 841
DB      860  TAACTGTGTAGATCTTATTGTCTATTTTTCCAAATTTATGACCCAGAAAAATA----- 911
QY      842  CAATAGGAAGAATAGTGGCATTAAAACTGAACCTTACAAGAGAGAAATTTTATACAACCTGAA 901
DB      912  -----TCAATAGAGGATTAATCTGAACCTTACACAGAGAAATTTTATACGATGTTA 961
QY      902  TAAATTTTGACCGTCTTACTTACCTTGAATTTCAACCCCAATCTCGCTATAATGGAATATA 961
DB      962  -----ATTGATATACATTTTAGAACCAATAACAGAACTAGAAA 997
QY      962  ATTAAACACGTTTCAGGGCTTAGATTTTTCATTTTTCATTTTAGATGAACTTATATTTTATACAA 1021
DB      998  ATGGATTAACTAGAAATCCTACATTTATTCTTGGATAAACCAAGGGCGTTTTACACAA 1057
QY      1022  AAAATGAAACGTACGGGAATCGTTTAGTTGGTATTTCGGAATCGTAAATAGATCTACTTATG 1081
DB      1058  GAAATCTCGAGACATCTTGTATCCTTATGATATTTTCTTTTACAGGTAAACCATGG 1117
QY      1082  CTACGACAGGAACCTGAAATTTATATATGGAGAAAGAACAGGTCCACCACCAACAAACAACTT 1141
DB      1118  CCTTTAGACATACTAATGATGATCGCAACATAATCTGGGGAGCGGTTTCATGGACATATTA 1177
QY      1142  TAATACCATTTGAATCTTATAAAGTTTCAATTTGTAACGTAGATAGACAAAGTAACTCCTACTT 1201
DB      1178  TTTCTCAAGACACATCCAAAGTATTTCCTTTTATAGAAACAAACCTATTGTGAAGGTG 1237
QY      1202  CCCCTTTTCTAAACATATACTTTTACAAATTAATCAAAATGAACTTTTATTTAAATAATTTAC 1261
DB      1238  AAATTTGTCAGACATAGAGGACTACTCAGATATATATATGAAATGATATTTTTCGAAATA 1297
QY      1262  CTAGTAATAAAATTAACATATTCAGCTGGGGGAAATTTTATCTAATGATAAAAAACAACTG 1321
DB      1298  GCAGTGAAGTATTTTCGATTTTTCATCCAATTAACAAATAGAAAAATAATTTATAAAGAACTG 1357
QY      1322  ATTTTCAATTTCTGTAAAAAAGACTGTAAACCAATTTAATCCAAATTTGTTTACCAA 1381
DB      1358  ATTTCTTATATGATCCAAACAAACATGGAATAAATAAGAAATATGTCATACTCTATCGT 1417
QY      1382  GCTATAATAGTTATAGTCAATTTTATCCAGTTTCTTTTATTTAATTTTCTTATATAAAA 1441
DB      1418  ATATAAAACTGATTAATATATATTTTC----- 1445
QY      1442  TTGGATTAGCGCTAAATATTTATATACAGGTGCAATTTAGGATGGACACACAGTAGTGTTA 1501
DB      1446  -----AGTAGTTAGAGAAAGAAAGAGATTGTCATTTAGTTGGACACATACTAGTGTG 1498
QY      1502  ATAGAAATTAATCCATATACAGATAAATAATTAATTTACATGATCCAGCAATCAAGGTTAACA 1561
DB      1499  ATTTCCAAATAACATAGATTTAGATAACATCACCCAAATCCACGCTCTAAAGGCTTTGA 1558
QY      1562  GTCTTGATACAAACTCTAAGGTAAATTTGAAGGACCTGGTTCATACAGGAGGAAACTTGGTTT 1621
DB      1559  AGGTAAGTTCTGATTTGAAATTTGTGAAAGGCTCTGGTCACACAGGTGGAGACTTGGTAA 1618
QY      1622  ATTTCAAAAGTCAAGGGCGTTTAGAGATTTACATGATAGAACTCCTTAATTTCTACAAATCTT 1681
DB      1619  TTTCTAAAGATAGTAGTGGATTTTAGAGTTAGATTTTAAAAAATGTTTCTCGACAAAT--- 1675
QY      1682  ATTACATTAGACTTCGATACGCTACAAATGGTGTGGAAATACTCTTCCATATATATCTC 1741
DB      1676  ATCAAGTAGCTATTCTGTTATGCTTAATGCTCCAAAGACAAACAGTA--TTCTTAACCGG 1733
QY      1742  TTACAATACCGAGGTAAATAGGAATAACCACTTCAACGACTCAACACACTTTTCTCGGTA 1801
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Db 1734 AATAGATACTATAAGTGTGGAGCTCCCTAGTACCACTTCCGCCAAAAC-----C 1783
Qy 1802 CAAATATTATAATTTACAAATCGGAGATTTTGGGTATTTCCAAATTTCCAAGTACAGT-- 1859
Db 1784 CAAATGCTACAGATTTAAACATATGCGAGATTTTGGATATGTAACATTTCCAAAGAACAGTTC 1843
Qy 1860 -----AACATTACCTTTAAATCGAACAATACCATTTATTTAATCGTGCAGATGTAT 1912
Db 1844 CAAATAAACAATTTGAAGGAGAGACACTTTTATTAATGACCTTATATGGTACCAAAATC 1903
Qy 1913 CAAATCAATTTTAAATCAATGATAAAATTTGAAATTTTATACCAATTTCTCTGTAGGCC 1972
Db 1904 ATTCAATATATATATATTTGACAAATCGAATTTTCCAACTCAATCTGTATTAG 1963
Qy 1973 AAAATAGAGAAAAACAAAATTTAGAAATCTCCAAACAAAATAAATACATTTTTCACAA 2032
Db 1964 ATTATACAGAGAGCAAAATATAGAAAAACACAGAAAAATAGTGAATGATTTATTGTGA 2023
Qy 2033 ATCATACAAAATACTTTTAAATATAGA 2060
Db 2024 ATTAAAACAAAGTCTTTACTAAAAATAGA 2051

RESULT 4

PCT-US94-07902-30
; Sequence 30, Application PC/TUS9407902
; GENERAL INFORMATION:
; APPLICANT: 4980 Carroll Canyon Road
; APPLICANT: Street address:
; APPLICANT: City: San Diego
; APPLICANT: State/Province: US
; APPLICANT: Country: California
; APPLICANT: Postal code/Zip: 92121
; APPLICANT: Phone number: (619) 453-8030 Fax number: (619) 453-6991
; APPLICANT: Telex number:
; TITLE OF INVENTION: Materials and Methods for the Control of
; TITLE OF INVENTION: Calliphoridae Pests
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07902
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US94-07902-30

Query Match 7.6%; Score 158; DB 6; Length 2061;
Best Local Similarity 48.3%; Pred. No. 4.3e-22;
Matches 999; Conservative 0; Mismatches 895; Indels 174; Gaps 13;

Qy 2 TGTGTCACGGGAATACACAATATGGTGATAATTTTCGAGACATTTGCTAGTGTGATACAA 61
Db 149 TGTGTCAGATATCAACAATATGGCAATATGCGGGGAATTTTGTAGTCTTGAAACTA 208
Qy 62 TTGCTGCAGTATAGTGCAGGTACTATTGTATCCGGTACTCTGTGTAGCCGGTATAGGTGGC 121
Db 209 TTGTTGGAGTATAGTGCAGGTATTATTGTAGTAGGAATCTATGTAGGAGCTTTTGTGCCC 268
Qy 122 TCACCTCTATATCCGACCGATAGGAATTAATAGGTGCTATTAATAATATCTTTTGTGATACC 181
Db 269 -----CTGTCTTAGCTGAGGTATATCTTTTGGGACTT 304
Qy 182 TAACTCACTGTCTTTTGGCCGCGGAGAACAAACAGATATGGACACAAATTTTATTA 241
Db 305 TGTGTCGATCTTTTGGCAAGGATCTGACCCCTG---CAAATGTTGCGAGATTTGTAA 361
Qy 242 AAATGGGAGAAATTTTGTGTATACACCGTTTAAACAGAAACATATAAAGCCTAAAGTTAC 301
Db 362 ACATCGGAGGAGCCCTATACAAAGAAATAGATAAAACATAATTAATGTACTAACTT--- 418
Qy 302 AAATTTTAGAAGGATTTAGCAAAATATTACAAAGCTATATACAGCAATTAGATGATTGA 361
Db 419 ---CTATCGTAAACACCTTATAAAATAATCAACTTGATTAATATCAAGAAATTTTTCGATAAT 475
Qy 362 GAAAAATTAAGAGACTACAAAGCTCTCGGATTACCAACCATCATCAGCAATTACAACAGCTG 421
Db 476 GGGAGCCAGCAGTACACACGCTAATGCTAAAGCAGTA-CATGATCTCTTTTACTACCTTA 534
Qy 422 CTTGACTCTTAAATAACGATTTTGAGAAATGTTTCAAAATGATTTTATTCGAGAAATACCTG 481
Db 535 GAACCTATATAGATAAAGATTTTAGATATGTTAAAAA----- 571
Qy 482 GTTTCGAACCTTGAACCTTATAAAGCGTATTACTACCTATTATTCGCAAGCTCTAATT 541
Db 572 -----ATAATGCTAGCTATCGAATACCAACACTCCCTCGCATATGCAAAATAGCTACTT 625
Qy 542 TTCAATTTAAATTTTATCAACAAGGTGCTGAAATGGCTGATGAATGGAATGCAGATATAC 601
Db 626 GGCACITGAAATTTTATTAACAATGCTGCTACTCTATTAACAATATATGCTGCAAAATCAAG 685
Qy 602 ATCCTTCACAAATTTGAACCTTAATGCTGGAACATCAGATGACTATTATAAACTTTTAAAG 661
Db 686 GT-----ATAAATCCAAGTACTTTCAATTCATCTAATTTACTACGGGCTATTAAAAAC 739
Qy 662 AAATATACCTTAATATATAGTAATCTATTGTCGAATACCTATAGAGAGGACTAATAAAC 721
Db 740 GTAAATATCAAGAATATATGACTATTGTTATACAAACGTACAATGCAGGACTAACTATGA 799
Qy 722 TTCGAACGACCTTAATATGAGATGGAGTATTTAATGATTATCGAAGATATATGACTA 781
Db 800 TTGACTTAATATACGCAACATGGAATATGTAATATATCTTACCGTTTAGAATGACTC 859
Qy 782 TTACTGTATTAGATACTATCGCTCAATTTTCTTTTATGATATATAAGAGATACAAAGATT 841
Db 860 TAACTGTGTTAGATCTTTATGCTATTATTTTCCAAATTTATGACCCAGAAAAATA----- 911
Qy 842 CAATAGGAAGAAATAGGTGGCAATTTAAACTGACCTTCAAGAGAAATTTATACAACTGAAA 901
Db 912 -----TCCAATAGGAGTTTAAATCTGAACCTTACCAGAGAAAGTTTATACGAATGTTA 961
Qy 902 TAAATTTTGACCGTCTTACTTACCTTGAATTTCAACCAATCTCGCTATAATGAATATA 961
Db 962 -----ATTCAGATACATTTAGAACCAATACAGAACTAGAAA 997
Qy 962 ATTTAAACACGTTCAAGGCTTAGATATTTTCAATTTTATAGATGAACCTTATATTTATACAA 1021
Db 998 ATGGATTAACCTAGAAATCTTACATTTATTTCTTGGATAAACCAAGGGCGTTTATACACAA 1057
Qy 1022 AAAATGAAACGTACGGGAATCGTTTGTGATTTGGAATCGTAATAGATCTACTTATG 1081
Db 1058 GAAATTCGAGACATCTTCTGATCCTTATGATATATTTTCTTTTACAGGTAAACGAGATGG 1117

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QY 1082 CTACGACAGAACTGAAATATATATATATGAGAAAGAACAGGTCCACCACACAAACAACTT 1141
Db 1118 CTTTACACATCTAATATGATGATCGCAACATAATCTGGGAGCGGTTCTATGGACATATTA 1177
QY 1142 TAATACATTTGAATCCTTAAGTTTCAATTTGTAATCTGATAGACAAAGTAACCTCTACTT 1201
Db 1178 TTCTCAAGACACATCCAAAGTATTTCCCTTTTATAGAAACAAACCTATTTGATAGGTG 1237
QY 1202 CCCCTTTTCTTAACATATCTTTACAAATTAATCAAAATGAACCTTTTATTAATAATTCAC 1261
Db 1238 AAATGTCAGACATAGAGAGTACTCAGATATATATATGAAATGATATTTTTCGAATA 1297
QY 1262 CTAGTAATAAATTAACATATTCAGCTGGGGGAAATTTATCTAATGATAAAACAACTG 1321
Db 1298 GCAGTGAAGTATTTTCGATATTCATCCAAATTCACCAATAGAAAATAATTTATAAGAACTG 1357
QY 1322 ATTTTCAATTTCTGTAAAAAAGAGCTGTAAACCAATTTAATCCAAATTTGTTTACCAC 1381
Db 1358 ATTCATTATGATCCAAAACAACATGGAAAATAAGAAATATGTCATCTACTATCTG 1417
QY 1382 GCTATTAATAGTTATAGTCATATTTTATCCAGTTTCTTTTATTAATTTTCTTATPAAA 1441
Db 1418 ATATAAAACTGATAATATATATTTTC----- 1445
QY 1442 TTGGATTAGCGCTAAATATATATATATACAGGTGCATTAGATGGACACACAGTAGTTTA 1501
Db 1446 -----AGTAGTTAGAGAAAGAGAGTTGTCATTTAGTTAGGACACATCTAGTGTG 1498
QY 1502 ATAGAAATATGCAATATCAGATAAAATAATACAAATGATCCAGCAATCAAAAGGTAAAC 1561
Db 1499 ATTCBAAAATACNATAGATTAGATAACATCACCCAAATCCAGCTCTAAAGCTTTGA 1558
QY 1562 GTCTTGATACAACTCTAAGGTAATTTGAAGGACCTGGTCATACAGAGGAACTTTGGTTT 1621
Db 1559 AGTAAAGTTCTGATTCGAAATTTGTGAAAGTCTCGTCACACAGGTGGAGACTTGGTAA 1618
QY 1622 ATTTACAAAGTCNAGCGGTTTAGAGATTACATGTAGAACTCTTAATTTCTACACATCTT 1681
Db 1619 TTCTTAAGATAGTATGGATTTTAGAGTTAGATTTTAAATAATGTTTCTCGACAAAT--- 1675
QY 1682 ATTACATTAGACTTCGATACGCTACAAATGGTCTGGAATACTCTTCCTAATATATATCTC 1741
Db 1676 ATCAAGTACGTATTCGTTATGCTACTACTATGCTCCAAAGACACAGTA--TTCTTAACCG 1733
QY 1742 TTACAATACAGAGTAATAGGAATACCACTCAACGACTCAACACACTTTTCTGGTA 1801
Db 1734 AATAGATACTATAAGTGTGGAGCTCCCTAGTACCCTCCCGCCAAAC-----C 1783
QY 1802 CAAATTAATAATTTACATACGGAGATTTGGGTATTTCCCAATTTCCCAAGTACAGT-- 1859
Db 1784 CAAATGCTACAGATTTAACATATGCAGATTTTGGATATGTAACATTTCCAAAGAACAGTTC 1843
QY 1860 -----AACATTACCTTTTAAATCGAAACATACCATTTATTTAATCGTGAGATGTAT 1912
Db 1844 CAAATTAACATTTGAGAGAGACACTTTTATATGACCTTATATGTTAGTACCAAAATC 1903
QY 1913 CAAATTTCAATTTAATCATGTATGATAAATTTGAATTTATACAAATTTCTCTGTACGCC 1972
Db 1904 ATTCAATAATATATATATTTGACAAATTTGAATTTTGGATATGTAACATTTCCAAAGAACAGTTC 1963
QY 1973 AAATAGAGAAACAAATTTAGAACTATCCAAACAAATTAATACATTTTTCACAA 2032
Db 1964 ATTATACAGAGAAAGCAAAATATAGAAAACACAGAAAATAGTGAATGATTTTATTTGTTA 2023
QY 2033 ATCATACAAAATACTTTTAAATATAGA 2060
Db 2024 ATTAAACAAAGTTCTTACTTAAATAGA 2051
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RESULT 5
US-08-315-468-3
; Sequence 3, Application US/08315468
; Patent No. 5554534

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; GENERAL INFORMATION:  
; APPLICANT: Michaels, Tracy Ellis  
; APPLICANT: Foncerrada, Luis  
; APPLICANT: Narva, Kenneth E.  
; TITLE OF INVENTION: Process for Controlling Scarab Pests  
; TITLE OF INVENTION: with Bacillus thuringiensis Isolates  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/315,468  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/014,941  
; FILING DATE: 01 FEB 1993  
; APPLICATION NUMBER: 07/828,430  
; FILING DATE: 30-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/808,316  
; FILING DATE: 16-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: MA73.C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3507 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis  
; STRAIN: kumamotoensis  
; INDIVIDUAL ISOLATE: 50C  
; IMMEDIATE SOURCE:  
; LIBRARY: LambdaGEM-11(tm) library of L. Foncerrada  
; CLONE: 50C(b)  
; US-08-315-468-3
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Query Match 4.4%; Score 92.6; DB 2; Length 3507;  
Best Local Similarity 44.7%; Pred. No. 3.5e-09;  
Matches 683; Conservative 0; Mismatches 784; Indels 60; Gaps 6;  
  
QY 429 TCTTAAATACGATTTGAGAAATGTTTCAATGATTTTATTCGAGAAATACCTGGTTTCCA 488  
Db 504 TGTTCGAATCGATTTGAAATCCTCGATGATTTATTTACGCAATATATGCCATCTTTTCG 563  
QY 489 ACTTGAAACTTATAAAACGCTTATTACTACCTATTTATGCGCAAGCTGCTAAATTTTCATT 548  
Db 564 AGTGACAAATTTTGAAGTACCATTCTTACAGTATATACAAATGGCAGCAAACTACATT 623  
QY 549 AAATTTATTACAAAGGTGCTGAATTTGCTGATGAATGGAATGCAGATATACATCTTC 608  
Db 624 ACTTTTATTAAGGGAGCGCATCAATTTTGGAGAAGAATGG----- 663  
QY 609 ACAAATTTGAACCTAATGCTGGAAACATCAGATGACTATTATATAAACTTTTAAAGAAATAT 668
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Db	664	-----GGATTGCTTCAAGCACTATTAACTACTTATCTGCTCAATGAACTTAC	1716
Qy	669	ACCTAATATAGTAATCTTGTGCAAACTCTATAGAGAGGACTTAAATAACTTCGAAA	728
Db	717	TGCAGAAATTTCTGACCACTGTGTAAGTGGTATGAACTGGTTTACGAAAATTAAGG	776
Qy	729	CGAACCTAATAGATGGAGTATATTAAATGATATCGAAGATATATGACTATTACTGT	788
Db	777	CTCGAGCGCTAAACAATGGGATGACTATAACCAATTCGCTAGAGAAATGACATGCGGT	836
Qy	789	ATTAGATACCTATCGCTCAATTTCTTTTATGATATAAAGAGAGATCAAGAATTCATPAGG	848
Db	837	GTTAGAGCTGTTGCAATTTTTCMAACTATGATACGCGTACGT-----ATCCACTGGC	890
Qy	849	AGAAATAGGTGGCATTTAAACTGAACTTCAAGAGAAATTTATACAACTGAAATTAATTT	908
Db	891	AACAACAGCTCAGCTTACAAGGGAAGTATATACAGATCCACTTGGCGCGTAGATGTGCC	950
Qy	909	TGACCGCTTACTTACCTTCAAAATTCACCCCAATCTCGCTATATGAAATATAATTTAAC	968
Db	951	TNATATTGGCTCTGGTATGACAAAGCACCTCTCTTCTCAGAAATAGAAAAGCGGTAT	1010
Qy	969	ACGTTACGGCTTAGATTAATTTTCAATTTTAGATGAATCTTATTTTATACAAAAATGA	1028
Db	1011	TCGTCCACCTCATG---TGTTGATATATATAACGGGACTCACAGTTTATACAAAAACG	1067
Qy	1029	AACGTACGGGAATCGTTAGTTGGTATTTGCGAATCGTAATAGATCTACTTATGCTAGAC	1088
Db	1068	TAGCTTCACT--TCTGATCGTTATGATGATATTGGGCTGTCTCATCAATAAGCTATAAG	1125
Qy	1089	AGGAATGAAATATATATGAGAGAAAGACAGGTCCACCCACACAAACAACTTTAAATCC	1148
Db	1126	CATATCGGTACGAGTAGTACCTTTTACACAGATGATGGAACCAATCAAAATTTACAAGT	1185
Qy	1149	ATTTGAATCTTATAAAGTTTCAATTTGTAATGATAGACAAAGTAATCTCTCTCCCTTT	1208
Db	1186	ACTAGCAATTTTGAATTTTACGAAATAGCATATTTTACAGACTTTTCAATGGTGCAGTA	1245
Qy	1209	TCCTAACATATACATTTTCAATTAATCAAAATGAACTTTTATTAATAATTCACCTAGTAA	1268
Db	1246	CTCCTGATATAGTTTACCCTGGTTATAGGTATACATTTTGTGAATGCCAGAAACCGAG	1305
Qy	1269	TAAATTAACATATTCAGCTGGGGGAATTTATCTAATGATATAAAAAACAATGATTTTCA	1328
Db	1306	TTTTTTATGGTAAATCAATTTGAATATACCAAGAAAGCGTTAACGTATAAACACGCTTC	1365
Qy	1329	ATTTCTGTAAAAAAGACTGTAAACCAATTTATTAATCCAAATTTTACCAGCTATAA	1388
Db	1366	AA-----AGATATTATAGATCGGACAGAGATTCGGAATTAGAATTCCTCAGAACTTC	1421
Qy	1389	TAGTTATAGTCATATTTTATCCAGTTTCTTTTATTTAATTTTCTTATAAAATGGATT	1448
Db	1422	AGGTCACCAATTTACGAGTCATATAGCCATAGATTAGGTCTATATTAATTTTACTC	1481
Qy	1449	AGCGTAAATATATATATACAGGTGCATTTAGGATGGACACACAGTAGTGTATAGAAA	1508
Db	1482	CAGTTTCACTAGCAGTATGTACCTGTATTTCTTGGACACATCGGAGTCGAGATCTAAC	1541
Qy	1509	TAAATGCAATATCAGATTAATAATTTACAAATGATCCAGCAATCAAAAGGTAACAGCTTGA	1568
Db	1542	AAATACAGTTAAAGTGGCGAAATCACCNAATACAGGGGCAAGTCTAGCACCATAGG	1601
Qy	1569	TACAACTCTAAGGTAATTTGAAGGACCTGGTGCATACAGGAGGAACTTTGGTTTATTACA	1628
Db	1602	CAGAAATCTTATATAATAAAGGCGGTGTTATACAGGGGAGACTTAGTGGCTTTAAC	1661
Qy	1629	AAGTCAAGGGCGTTTAGAGATTAATGATAGAACTCTTAATTCACAAATCTTATACAT	1688
Db	1662	GGACCGCATCGGAAGTTGTGAGTTTTCAGATGATCTTTCCAGAGTCTCAACGATCCGAT	1721
Qy	1689	TAGACTTCGATACCGTACAAATGGTGTGGAAATCTCTCTCTAATATATCTCTTACAAT	1748
Db	1722	TCGGATTGCTTAGCTTCTTAATGAACTAGTTATA-----TTAGTTT	1763
Qy	1749	ACCAGAGTAATAGGAATACCCTCAACGACTCAACAAACACTTTTCTGGTACAAATTA	1808
Db	1764	ATAGGACTTAACCAAGCGGAACTTTAAATTTCAACGACATATTTCTAATAAAATGA	1823
Qy	1809	TAATAATTTACAAATACGGAGATTTTGGGTATTTTCCAAATTTTCCAAATGACAGTAACTTACC	1868
Db	1824	AAATGATTTAACATATAATGATTTTCAATATATAGAAATATCCAAAGAGTCAATTTTCAGTAA	1883
Qy	1869	TTTAAATCGAAACATACCCTTTATATTTTAAATCGTGCAGATGATCAAAATTCAAATTTTAAAT	1928
Db	1884	TGCTTCTTCAACATACAGAGGTTTCTATATAGTATACAAACGAATTAATTTATTTAT	1943
Qy	1929	CATTGATAAAATGAAATTTTATACCAAT	1955
Db	1944	TTTAGCCGATCGAATTCATCCAGT	1970

RESULT 6

US-08-349-867-22
; Sequence 22, Application US/08349867
; Patent No. 5508264
; GENERAL INFORMATION:
; APPLICANT: Bradfisch, Gregory A.
; APPLICANT: Thompson, Mark
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: No. 5508264el Pesticidal Compositions
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,867
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA86
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-349-867-22

Query Match 3.8%; Score 79.6; DB 2; Length 3444;
Best Local Similarity 53.3%; Pred. No. 1.3e-06;
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;
Qy 436 ATACGATTGAGAAATGTTTCAAAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGA 495
Db 388 ATTCGATTGCTTAATACAGAGCGCTTTAATAACAGCAATAATAATTTTACACTTACA 447
Qy 496 ACTTATAAAACGCTTATTTACTACTTATTTATCGCAAGCTGCTAATTTTCAATTAATTA 555
Db 448 AGTTTGAATCCCTCTTTTATCGCTGTATGTTCAAGCGGGAATTTACATTTTACTACTA 507

QY	496	ACTTATAAACGCTATTACTACTATTTATGCGCAGCTGCTAAATTTTTCATTTTAAATTTA	555
Db	448	AGTTTTGAAATCCCTCTTTTATCGGCTATGTTCAAGCGCGGAATTTTACATTTATCACTA	507
QY	556	TTACAACAAGGTGCTGAATTTGGCTGATGAATGGAATGCGAGATATACATCCTTCACAAAAT	615
Db	508	TTAAGAGAGCGCTGATCGTTTGGCAGGGTTGGGAGCTGATATAGCTACTGTTAATAAT	567
QY	616	GAACCTAATGCTGGAACATCAGATGACTATTATAAATCTTTTAAAGAAAATATACCTAAA	675
Db	568	C-----ATTATAATAGATTATAATAATCTTTATTTCATAGA	600
QY	676	TATAGTAACCTATTGTCAAATACCTATAGAGAGGACTAAATAAACTTCGAAACGAACCT	735
Db	601	TATACGAAACATTTGTTGGACACATACATCAAGGATTAGAAAACCTTAAGAGGTACTAAT	660
QY	736	AATATGAGATGGAGTATATTAAATGATATCGAAGATATATGACTATTACTGTATTAGAT	795
Db	661	ACTCGACAATGGCAGAGTTCAATCAGTTTAGGAGAGATTTAACACTTACTGTATTAGAT	720
QY	796	ACTATCGCTCAATTTCTTTTATGATATAAAGAGATA	833
Db	721	ATCGTTGCTCTTTTCCGAACTACGATGTAGAACATA	758
RESULT 9			
US-08-239-476-26			
; Sequence 26, Application US/08239476			
; Patent No. 5527883			
; GENERAL INFORMATION:			
; APPLICANT: Thompson, Mark			
; APPLICANT: Schwab, George E.			
; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in			
; TITLE OF INVENTION: Pseudomonas fluorescens			
; NUMBER OF SEQUENCES: 34			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: David R. Saliwanchik			
; STREET: 2421 N.W. 41st Street, Suite A-1			
; CITY: Gainesville			
; STATE: Florida			
; COUNTRY: USA			
; ZIP: 32606			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/239,476			
; FILING DATE:			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Saliwanchik, David R.			
; REGISTRATION NUMBER: 31,794			
; REFERENCE/DOCKET NUMBER: MA83			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (904) 375-8100			
; TELEFAX: (904) 372-5800			
; INFORMATION FOR SEQ ID NO: 26:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 3444 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: DNA (genomic)			
US-08-239-476-26			
Query Match 3.8%; Score 79.6; DB 2; Length 3444;			
Best Local Similarity 53.3%; Pred. No. 1.3e-06;			
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;			
QY	436	ATACGATTGAGATGTTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAA	495

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Query Match          3.8%; Score 79.6; DB 2; Length 3444;
Best Local Similarity 53.3%; Pred. No. 1.3e-06;
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

QY 436 ATACGATTGGAAGTTCACAAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAA 495
DB 388 ATTCGATTGCTATACAGACGAGCTTTAAATACAGCAATAAATAATTTTACACTTACA 447
QY 496 ACTTATAAACGCTATTACTACTATTTATGCGCAAGCTGCTAAATTTTCATTAAATTTA 555
DB 448 AGTTTTGAAATCCCTCTTTTATCGGCTATGTTCAAGCGCGCAATTTACATTTATCACA 507
QY 556 TTACACAACAGGCTGCTGAATGCTGATGATGGAATGCGATATACATCCITTCACAAAT 615
DB 508 TTAAGAGACGCTGTATCGTTTGGGACGCTGGATATAGCTACTGTTTAATAAT 567
QY 616 GAACCTAATGCTGGAACATCAGATGACTATATAAACTTTTAAAGAAAATATACCTAA 675
DB 568 C-----ATTATATAGATTAATAAATCTTATTCATAGA 600
QY 676 TATAGTAATCTATGTGCAAAATACCTATAGAGAGGACTAAATAAACTTCGAAACGAACT 735
DB 601 TATACGAAACATGTTTGGACACATACAATCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660
QY 736 AATATGAGATGAGATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGAT 795
DB 661 ACTCGACAAATGGCAAGATTCAATCAGTTTAGGAGAGATTAAACACTTACTGTATTAGAT 720
QY 796 ACTATCGCTCAATTTCTTTTATGATATAAAGAGATA 833
DB 721 ATCGTTGCTCTTTTCCGAACTACGATGTAGAACATA 758

RESULT 11
US-08-598-305A-26
; Sequence 26, Application US/08598305A
; Patent No. 5827514
; GENERAL INFORMATION:
; APPLICANT: BRADFISCH, Gregory A.
; APPLICANT: THOMPSON, Mark
; APPLICANT: SCHWAB, George E.
; TITLE OF INVENTION: No 5827514e1 Pesticidal Compositions
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/598,305A
; FILING DATE: 08-FEB-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/349,867
; FILING DATE: 06-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA86.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-598-305A-26

Query Match          3.8%; Score 79.6; DB 2; Length 3444;
Best Local Similarity 53.3%; Pred. No. 1.3e-06;
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

QY 436 ATACGATTGGAAGTTCACAAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAA 495
DB 388 ATTCGATTGCTATACAGACGAGCTTTAAATACAGCAATAAATAATTTTACACTTACA 447
QY 496 ACTTATAAACGCTATTACTACTATTTATGCGCAAGCTGCTAAATTTTCATTAAATTTA 555
DB 448 AGTTTTGAAATCCCTCTTTTATCGGCTATGTTCAAGCGCGCAATTTACATTTATCACA 507
QY 556 TTACACAACAGGCTGCTGAATGCTGATGGAATGCGATATACATCCITTCACAAAT 615
DB 508 TTAAGAGACGCTGTATCGTTTGGGACGCTGGATATAGCTACTGTTTAATAAT 567
QY 616 GAACCTAATGCTGGAACATCAGATGACTATATAAACTTTTAAAGAAAATATACCTAA 675
DB 568 C-----ATTATATAGATTAATAAATCTTATTCATAGA 600
QY 676 TATAGTAATCTATGTGCAAAATACCTATAGAGAGGACTAAATAAACTTCGAAACGAACT 735
DB 601 TATACGAAACATGTTTGGACACATACAATCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660
QY 736 AATATGAGATGAGATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGAT 795
DB 661 ACTCGACAAATGGCAAGATTCAATCAGTTTAGGAGAGATTAAACACTTACTGTATTAGAT 720
QY 796 ACTATCGCTCAATTTCTTTTATGATATAAAGAGATA 833
DB 721 ATCGTTGCTCTTTTCCGAACTACGATGTAGAACATA 758

RESULT 12
US-08-639-923A-22
; Sequence 22, Application US/08639923A
; Patent No. 5840554
; GENERAL INFORMATION:
; APPLICANT: Thompson, Mark
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
; TITLE OF INVENTION: Pseudomonas fluorescens
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,923A
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,476
; FILING DATE: 06-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA83.D1
```



```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-639-923A-22

Query Match      3.8%; Score 79.6; DB 2; Length 3444;
Best Local Similarity 53.3%; Pred. No. 1.3e-06;
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

QY 436 ATACGATTGGAGATGTTCAATGATTTTATTCGAGAAATACCTGGTTCCCACTTGAA 495
Db 388 ATTCGATTGCTAATACAGACGCGCTTTAATACAGCAATAAATAATTTTACACTTACA 447
QY 496 ACTATATAAAGCGTATTACTACCTATTATGCGCAAGCTGCTAATTTTCAATTTAAATTTA 555
Db 448 AGTTTGAATCCCTCTTTTATCGGCTATGTTCAAGCGGCGAATTTTACATTATCTACA 507
QY 556 TTACAACAAGGTGCTGAATGGCTGATGGAATGGAATGCAGATATACATCTTCACAAATT 615
Db 508 TTAAGAGACGCTGATCGTTGGCAGGTTGGGACTGGATATAGCTACTGTTAATAAT 567
QY 616 GAACCTAATGCTGGAACATCAGATGACTATTATATAACTTTTAAAGAAATATACCTAAA 675
Db 568 C-----ATTATAATAGATTAATAAATCTTTATTCATAGA 600
QY 676 TATAGTAACCTATTGTGCAATACCTATAGAGAGAGGACTAAATAAATCTCGAAACGACCT 735
Db 601 TATACGAAACATATGTTTGGACACATCAATCAAGGATTAGAAACTTAAGAGGTACTAAT 660
QY 736 AATATGAGATGGAGTATTTAATTAATGATTCGAAGATATATGACTATTACTGTATTAGAT 795
Db 661 ACTCGAATGGGCAAGATTCATCAGTTTAGGAGAGATTTAACAATCTACTGTATTAGAT 720
QY 796 ACTATCGCTCAATTTCTTTTATGATATATAAGAGATA 833
Db 721 ATCGTTGCTCTTTTCCGAACTACGATGTAGAACATA 758

RESULT 13
US-08-639-923A-26
; Sequence 26, Application US/08639923A
; Patent No. 5840554
; GENERAL INFORMATION:
; APPLICANT: Thompson, Mark
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
; PSEUDOMONAS FLUORESCENS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,923A
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,476
```

```
; FILING DATE: 06-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA83.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-639-923A-26

Query Match      3.8%; Score 79.6; DB 2; Length 3444;
Best Local Similarity 53.3%; Pred. No. 1.3e-06;
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

QY 436 ATACGATTGGAGATGTTCAATGATTTTATTCGAGAAATACCTGGTTCCCACTTGAA 495
Db 388 ATTCGATTGCTAATACAGACGCGCTTTAATACAGCAATAAATAATTTTACACTTACA 447
QY 496 ACTATATAAAGCGTATTACTACCTATTATGCGCAAGCTGCTAATTTTCAATTTAAATTTA 555
Db 448 AGTTTGAATCCCTCTTTTATCGGCTATGTTCAAGCGGCGAATTTTACATTATCTACA 507
QY 556 TTACAACAAGGTGCTGAATGGCTGATGGAATGGAATGCAGATATACATCTTCACAAATT 615
Db 508 TTAAGAGACGCTGATCGTTGGCAGGTTGGGACTGGATATAGCTACTGTTAATAAT 567
QY 616 GAACCTAATGCTGGAACATCAGATGACTATTATATAACTTTTAAAGAAATATACCTAAA 675
Db 568 C-----ATTATAATAGATTAATAAATCTTTATTCATAGA 600
QY 676 TATAGTAACCTATTGTGCAATACCTATAGAGAGAGGACTAAATAAATCTCGAAACGACCT 735
Db 601 TATACGAAACATATGTTTGGACACATCAATCAAGGATTAGAAACTTAAGAGGTACTAAT 660
QY 736 AATATGAGATGGAGTATTTAATTAATGATTCGAAGATATATGACTATTACTGTATTAGAT 795
Db 661 ACTCGAATGGGCAAGATTCATCAGTTTAGGAGAGATTTAACAATCTACTGTATTAGAT 720
QY 796 ACTATCGCTCAATTTCTTTTATGATATATAAGAGATA 833
Db 721 ATCGTTGCTCTTTTCCGAACTACGATGTAGAACATA 758

RESULT 14
PCT-US95-05431-22
; Sequence 22, Application PC/TUS9505431
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT: Street address: 5501 Oberlin Drive
; APPLICANT: City: San Diego
; APPLICANT: State/Province: California
; APPLICANT: Country: US
; APPLICANT: Postal code/Zip: 92121
; APPLICANT: Phone number: (619) 453-8030
; APPLICANT: Telex number:
; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
; PSEUDOMONAS FLUORESCENS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
```

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05431
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA83
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US95-05431-22

Query Match 3.8%; Score 79.6; DB 6; Length 3444;
Best Local Similarity 53.3%; Pred. No. 1.3e-06;
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

QY 436 ATACGATTTGAGAAATGTTTACCAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAA 495
DB 388 ATTCGATTTGCTTAATACAGACGCGCTTTTAATACAGCAATAAATAATTTTACACTTACA 447
QY 496 ACTTATAAAACGCTATTACTACCTATTATTCGCGAAGCTGCTAAATTTTTCATTAAATTTA 555
DB 448 AGTTTGAATCCCTCTTTTATCGGCTCTATGTTCAAGCGGCGAATTTACATTTATCACA 507
QY 556 TTACAACAAGGTGCTGAATGGCTGATGAATGGAATGCAGATATACATCCTTCACAAAT 615
DB 508 TTAAGAGACGCTGATCGTTTGGGCGAGGTTGGGAGCTGGATATAGTACTGTTAATAAT 567
QY 616 GAACCTAATGCTGGAAACATCAGATGACTATTATAAACTTTTAAAGAAATATACCTTAA 675
DB 568 C-----ATTATAATAGATTAATAAACTTTTATTCATAGA 600
QY 676 TATAGTAATATTGTGCAAAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACT 735
DB 601 TATACGAACATTTGTTGGACACATACATCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660
QY 736 AATATGAGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTTACTGTATTAGAT 795
DB 661 ACTCGACAATGGGCAAGATTCAATCAGTTTAGGAGAGATTTAACACTTACTGTATTAGAT 720
QY 796 ACTATCGCTCAATTTCTTTTATGATATAAAGAGATA 833
DB 721 ATCGTTGCTCTTTTCCGAACACTACGATGTTAGAACATA 758

RESULT 15
PCT-US95-05431-26
; Sequence 26, Application PC/TUS9505431
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT: Street address: 5501 Oberlin Drive
; APPLICANT: City: San Diego
; APPLICANT: State/Province: California
; APPLICANT: Country: US
; APPLICANT: Postal code/zip: 92121
; APPLICANT: Phone number: (619) 453-8030 Fax number: (619) 453-6991
; APPLICANT: Telex number:
; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
; PSEUDOMONAS FLUORESCENS
; NUMBER OF SEQUENCES: 34
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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05431
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA83
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US95-05431-26

Query Match 3.8%; Score 79.6; DB 6; Length 3444;
Best Local Similarity 53.3%; Pred. No. 1.3e-06;
Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

QY 436 ATACGATTTGAGAAATGTTTACCAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAA 495
DB 388 ATTCGATTTGCTTAATACAGACGCGCTTTTAATACAGCAATAAATAATTTTACACTTACA 447
QY 496 ACTTATAAAACGCTATTACTACCTATTATTCGCGAAGCTGCTAAATTTTTCATTAAATTTA 555
DB 448 AGTTTGAATCCCTCTTTTATCGGCTCTATGTTCAAGCGGCGAATTTACATTTATCACA 507
QY 556 TTACAACAAGGTGCTGAATGGCTGATGAATGGAATGCAGATATACATCCTTCACAAAT 615
DB 508 TTAAGAGACGCTGATCGTTTGGGCGAGGTTGGGAGCTGGATATAGTACTGTTAATAAT 567
QY 616 GAACCTAATGCTGGAAACATCAGATGACTATTATAAACTTTTAAAGAAATATACCTTAA 675
DB 568 C-----ATTATAATAGATTAATAAACTTTTATTCATAGA 600
QY 676 TATAGTAATATTGTGCAAAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACT 735
DB 601 TATACGAACATTTGTTGGACACATACATCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660
QY 736 AATATGAGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTTACTGTATTAGAT 795
DB 661 ACTCGACAATGGGCAAGATTCAATCAGTTTAGGAGAGATTTAACACTTACTGTATTAGAT 720
QY 796 ACTATCGCTCAATTTCTTTTATGATATAAAGAGATA 833
DB 721 ATCGTTGCTCTTTTCCGAACACTACGATGTTAGAACATA 758

Search completed: February 15, 2006, 03:31:12
Job time : 384 secs
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Db 181 CTAATCACTGTCTTTTGGCCGCGGAGAACAAAGACAAAACAGATATGGACACAATTTATT 240
Qy 241 AAAATCGGAGAAATTTTGTGTGATACACCGTTAAACAGAAAGCATAAAAACAGCTAAAGTTA 300
Db 241 AAAATCGGAGAAATTTTGTGTGATACACCGTTAAACAGAAAGCATAAAAACAGCTAAAGTTA 300
Qy 301 CAAACTTTAGAGGATTTAGACAAATTTTACAAGCTATAATACAGCATTAGATGATTGG 360
Db 301 CAAACTTTAGAGGATTTAGACAAATTTTACAAGCTATAATACAGCATTAGATGATTGG 360
Qy 361 AGAAATTTAAAGACTACAAGCTCTGATTTACCAACCATCATCAGCATTTACAACAAGCT 420
Db 361 AGAAATTTAAAGACTACAAGCTCTGATTTACCAACCATCATCAGCATTTACAACAAGCT 420
Qy 421 GCCTTGACTCTTTAAATACGAATTTGAGAAATGTTTACAANTGATTTTATTCGAGAAATPACCT 480
Db 421 GCCTTGACTCTTTAAATACGAATTTGAGAAATGTTTACAANTGATTTTATTCGAGAAATPACCT 480
Qy 481 GGTTCCTCACTTGAACCTTTAATAACGCTTACTTACCTATTATTTATGCGCAAGCTGCTAAT 540
Db 481 GGTTCCTCACTTGAACCTTTAATAACGCTTACTTACCTATTATTTATGCGCAAGCTGCTAAT 540
Qy 541 TTTTCATTTAAATTTATTAACAAGGTGCTGAATTCGCTGATGAATGGAATGCAGATATA 600
Db 541 TTTTCATTTAAATTTATTAACAAGGTGCTGAATTCGCTGATGAATGGAATGCAGATATA 600
Qy 601 CATCTTCAAAATGGAACCTAATGCTGGAACATCAGATGACTATTATTAACCTTTTAAAA 660
Db 601 CATCTTCAAAATGGAACCTAATGCTGGAACATCAGATGACTATTATTAACCTTTTAAAA 660
Qy 661 GAAATATACCTTAATATAGTAACTATTGTGCAAAATACCTATAGAGAAAGCACTAATAAA 720
Db 661 GAAATATACCTTAATATAGTAACTATTGTGCAAAATACCTATAGAGAAAGCACTAATAAA 720
Qy 721 CTTTCGAAACGAACCTAATATGAGATGAGTATTTAATGATTATCGAAGATATATGACT 780
Db 721 CTTTCGAAACGAACCTAATATGAGATGAGTATTTAATGATTATCGAAGATATATGACT 780
Qy 781 ATTACTGTATTAGATACTATCGCTCAATTTTCTTTTATGATATAAAGAGATACAAAGAT 840
Db 781 ATTACTGTATTAGATACTATCGCTCAATTTTCTTTTATGATATAAAGAGATACAAAGAT 840
Qy 841 TCAATAGGAAGATAGGTGGCATTAAACCTGAACCTTACAAGAAATTTATACAACTGAA 900
Db 841 TCAATAGGAAGATAGGTGGCATTAAACCTGAACCTTACAAGAAATTTATACAACTGAA 900
Qy 901 ATAAATTTTGACCGTCTTACTTACCTTGAAATTTCAACCCAACTCTCGCTATAATGGAATAT 960
Db 901 ATAAATTTTGACCGTCTTACTTACCTTGAAATTTCAACCCAACTCTCGCTATAATGGAATAT 960
Qy 961 AATTTAAACAGTTCAGGGCTTAGATTATTTTCAATTTTATAGATGAACCTTATTTATACA 1020
Db 961 AATTTAAACAGTTCAGGGCTTAGATTATTTTCAATTTTATAGATGAACCTTATTTATACA 1020
Qy 1021 AAAATGAAACGTACGGGAATCGTTAGTTGGTATTCGAAATCGTAATAGATCTACTTAT 1080
Db 1021 AAAATGAAACGTACGGGAATCGTTAGTTGGTATTCGAAATCGTAATAGATCTACTTAT 1080
Qy 1081 GCTACGACAGGAACCTGAAATTTATATGAGAAAGAAACAGGTCCACCCCAACAAAACCT 1140
Db 1081 GCTACGACAGGAACCTGAAATTTATATGAGAAAGAAACAGGTCCACCCCAACAAAACCT 1140
Qy 1141 TTAATAACCAATTTGAATCCTTAAAGTTTCAATTTGTAACCTGATAGACAAAGTAACTCTACT 1200
Db 1141 TTAATAACCAATTTGAATCCTTAAAGTTTCAATTTGTAACCTGATAGACAAAGTAACTCTACT 1200
Qy 1201 TCCCTTTTCCCTAACATATACCTTACAAATTAATCAAAATGGAATTTAATAATATTTCA 1260
Db 1201 TCCCTTTTCCCTAACATATACCTTACAAATTAATCAAAATGGAATTTAATAATATTTCA 1260
Qy 1261 CCTAGTAATAAATTAACATATTCAGCTGGGGGGAATTTATCTAATGATAAAAAACAACCT 1320
Db 1261 CCTAGTAATAAATTAACATATTCAGCTGGGGGGAATTTATCTAATGATAAAAAACAACCT 1320
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Qy 1321 GATTTTCAATTTCTCTGTAAAAAAGACCTGTAAACCAATTTATTAATCCAAATTTGTTTACCA 1380
Db 1321 GATTTTCAATTTCTCTGTAAAAAAGACCTGTAAACCAATTTATTAATCCAAATTTGTTTACCA 1380
Qy 1381 AGCTATAATAGTTATAGTCATATTTTATCCCAAGTTTCTTTATTTAAATTTCTCTATAAA 1440
Db 1381 AGCTATAATAGTTATAGTCATATTTTATCCCAAGTTTCTTTATTTAAATTTCTCTATAAA 1440
Qy 1441 ATTGGATTAGCGCTAAATATATATATATACAGGTGCATTAGGATGGACACACAGTAGTGT 1500
Db 1441 ATTGGATTAGCGCTAAATATATATATATATACAGGTGCATTAGGATGGACACACAGTAGTGT 1500
Qy 1501 AATAGAAATATGCAATATCAGATAAAAATATTAATCAATGATCCAGCAATCAAGGTAAC 1560
Db 1501 AATAGAAATATGCAATATCAGATAAAAATATTAATCAATGATCCAGCAATCAAGGTAAC 1560
Qy 1561 AGCTTTGATACAAACTCTTAAGGTAATTCGAAGCACTGGTTCATACAGGAGGAAACTTGGTT 1620
Db 1561 AGCTTTGATACAAACTCTTAAGGTAATTCGAAGCACTGGTTCATACAGGAGGAAACTTGGTT 1620
Qy 1621 TATTTACAAAGTCAAGGCGTTTAGAGATTACATGTAGAACTCTTAATTTCTACAAATCT 1680
Db 1621 TATTTACAAAGTCAAGGCGTTTAGAGATTACATGTAGAACTCTTAATTTCTACAAATCT 1680
Qy 1681 TATTTACATAGACTTCGATACGCTACAAATGCTGCTGGAAATACCTCTTCTTAATATATCT 1740
Db 1681 TATTTACATAGACTTCGATACGCTACAAATGCTGCTGGAAATACCTCTTCTTAATATATCT 1740
Qy 1741 CTTACAATACCAAGGATTAATAGGAATACCACTCAACGACTCAACAACACTTTTTCTGT 1800
Db 1741 CTTACAATACCAAGGATTAATAGGAATACCACTCAACGACTCAACAACACTTTTTCTGT 1800
Qy 1801 ACAAAATTAATAATTTTACAATACGGAGATTTTGGTATTTTCCAAATTTCCAAAGTACAGTA 1860
Db 1801 ACAAAATTAATAATTTTACAATACGGAGATTTTGGTATTTTCCAAATTTCCAAAGTACAGTA 1860
Qy 1861 ACATTTACCTTTAAATCGAAACATACCAATTTATTTAATCGTGAGATGTATCAAAATTC 1920
Db 1861 ACATTTACCTTTAAATCGAAACATACCAATTTATTTAATCGTGAGATGTATCAAAATTC 1920
Qy 1921 ATTTTAACTCATTTGATAAAATTTGAATTTATACCAATTTACTTCTCTGTGACGCAAAATAGA 1980
Db 1921 ATTTTAACTCATTTGATAAAATTTGAATTTATACCAATTTACTTCTCTGTGACGCAAAATAGA 1980
Qy 1981 GAAAAACAAAATTAGAAAATATCCAAACAAAATAAATAATATTTTTCACAAATCATACA 2040
Db 1981 GAAAAACAAAATTAGAAAATATCCAAACAAAATAAATAATATTTTTCACAAATCATACA 2040
Qy 2041 AAAATACCTTTAAATATAGAGCCCAAACTATGATATTGATTAA 2085
Db 2041 AAAATACCTTTAAATATAGAGCCCAAACTATGATATTGATTAA 2085
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RESULT 2

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US-10-782-570-1
; Sequence 1, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; PRIOR FILING DATE: 2004-02-19
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 1
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2235)
US-10-782-570-1

Query Match      100.0%; Score 2085; DB 8; Length 2235;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2085; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTCAGGGAATACACAAATATGCTGATAATTTTCGAGACATTTCTAGTGTGCTGATACA 60
DB 151 ATGTGTCAGGGAATACACAAATATGCTGATAATTTTCGAGACATTTCTAGTGTGCTGATACA 210
QY 61 ATTGCTGCAGTTAGTCAGGTACTATTGTATCCGGTACTCTGTTAGCCGGTATAGGTGG 120
DB 211 ATTGCTGCAGTTAGTCAGGTACTATTGTATCCGGTACTCTGTTAGCCGGTATAGGTGG 270
QY 121 CTCACCTTCTATATCCGACCGATAGGAATAATAGGTGCTATATAATATCTTTTGTGACC 180
DB 271 CTCACCTTCTATATCCGACCGATAGGAATAATAGGTGCTATATAATATCTTTTGTGACC 330
QY 181 CTAATCACTGCTTTTGGCCCGGGGAGAACAGACAAACAGTATGGACACAAATTTATT 240
DB 331 CTAATCACTGCTTTTGGCCCGGGGAGAACAGACAAACAGTATGGACACAAATTTATT 390
QY 241 AANAATGGGAGAAATTTTGTGTATACACCGTTAACGAAAGCATATAACAGCTAAAGTTA 300
DB 391 AANAATGGGAGAAATTTTGTGTATACACCGTTAACGAAAGCATATAACAGCTAAAGTTA 450
QY 301 CAAACTTTAGAGGATTTAGACAAATATTAACAAAGCTATTAATACAGCATTTAGATGG 360
DB 451 CAAACTTTAGAGGATTTAGACAAATATTAACAAAGCTATTAATACAGCATTTAGATGG 510
QY 361 AGAAATTTAAAGAGACTACAAGCTCCCTGGATTACCAATCATCATCAGCATTAACAAGCT 420
DB 511 AGAAATTTAAAGAGACTACAAGCTCCCTGGATTACCAATCATCATCAGCATTAACAAGCT 570
QY 421 GCCTTGACTCTTAAATACGATTTGAGAAATGTTTACAAATGATTTTATTCGAGAAATACCT 480
DB 571 GCCTTGACTCTTAAATACGATTTGAGAAATGTTTACAAATGATTTTATTCGAGAAATACCT 630
QY 481 GGTTCCTCAACTTGAACTTTATTAACCGCTATTACTACTATTATGCGCAAGCTGCTAAT 540
DB 631 GGTTCCTCAACTTGAACTTTATTAACCGCTATTACTACTATTATGCGCAAGCTGCTAAT 690
QY 541 TTTTCATTTAAATTTATTACAAACAGGCTGCTGAAATGCGTGAATGGAATGCGAGATATA 600
DB 691 TTTTCATTTAAATTTATTACAAACAGGCTGCTGAAATGCGTGAATGGAATGCGAGATATA 750
QY 601 CATCCTTCAAAATGGAACCTTAATGCTGGACATCAGATGACTATTATAACTTTTAAAA 660
DB 751 CATCCTTCAAAATGGAACCTTAATGCTGGACATCAGATGACTATTATAACTTTTAAAA 810
QY 661 GAAATATACCTAAATATAGTAACTATTGTGCAAAATACCTATAGAGAAGGACTAAATAAA 720
DB 811 GAAATATACCTAAATATAGTAACTATTGTGCAAAATACCTATAGAGAAGGACTAAATAAA 870
QY 721 CTTTGGAAACGAACTTAATATGAGATGGAGTATATTTAATGATATTCGAAGATATATGACT 780
DB 871 CTTTGGAAACGAACTTAATATGAGATGGAGTATATTTAATGATATTCGAAGATATATGACT 930
QY 781 ATTACTGATTTAGATACCTATCGCTCAATTTTCTTTTATGATATATAAGAGATACAAAGAT 840
DB 931 ATTACTGATTTAGATACCTATCGCTCAATTTTCTTTTATGATATATAAGAGATACAAAGAT 990
QY 841 TCAATAGGAAGATAGGTGGCAATTAACAACTGAACCTTACAAGAGAAATTTTATACAACCTGAA 900
DB 991 TCAATAGGAAGATAGGTGGCAATTAACAACTGAACCTTACAAGAGAAATTTTATACAACCTGAA 1050
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QY 901 ATAAATTTTGACCGCTTACTTACCTTGAAATTCACCAATCTCGCTATATAGTAATAT 960
DB 1051 ATAAATTTTGACCGCTTACTTACCTTGAAATTCACCAATCTCGCTATATAGTAATAT 1110
QY 961 AATTTAAACACGTTTACGGCTTAGATATTTTTCATTTTATAGATGAACCTTATATTTATACA 1020
DB 1111 AATTTAAACACGTTTACGGCTTAGATATTTTTCATTTTATAGATGAACCTTATATTTATACA 1170
QY 1021 AAAAATGAAACGTTACGGGAATCGTTTAGTTGGTATTTCGGAATCGTAAATAGATCTACTTAT 1080
DB 1171 AAAAATGAAACGTTACGGGAATCGTTTAGTTGGTATTTCGGAATCGTAAATAGATCTACTTAT 1230
QY 1081 GCTACGACAGGAACGTGAAATTTATATATGAGAGAAAGAACAGGTCCACCCACACAAAACCT 1140
DB 1231 GCTACGACAGGAACGTGAAATTTATATATGAGAGAAAGAACAGGTCCACCCACACAAAACCT 1290
QY 1141 TTAATACCAATTTGAATCCTTATAAGTTTCAATTTGTAACTGATAGACAAAGTAACTCTACT 1200
DB 1291 TTAATACCAATTTGAATCCTTATAAGTTTCAATTTGTAACTGATAGACAAAGTAACTCTACT 1350
QY 1201 TCCCTCTTTTCTTAACATATCTTTTCAAAATTAATCAAAATGAACTTTTATTTAAATAATTTCA 1260
DB 1351 TCCCTCTTTTCTTAACATATCTTTTCAAAATTAATCAAAATGAACTTTTATTTAAATAATTTCA 1410
QY 1261 CCTAGTAATAAATAATTAACATATTCAGCTGGGGGAAATTTATCTAATGATATAAATAAATACT 1320
DB 1411 CCTAGTAATAAATAATTAACATATTCAGCTGGGGGAAATTTATCTAATGATATAAATAAATACT 1470
QY 1321 GATTTTCAATTTCTGTAAAAAAGAGCTGTAAACCAATTTAATCCAAATCTGTTTATACCA 1380
DB 1471 GATTTTCAATTTCTGTAAAAAAGAGCTGTAAACCAATTTAATCCAAATCTGTTTATACCA 1530
QY 1381 AGCTATAATAGTTATAGTCATATTTTATCCAGTTTCTTTTATTTAATTTATTTCTCTATAAA 1440
DB 1531 AGCTATAATAGTTATAGTCATATTTTATCCAGTTTCTTTTATTTAATTTATTTCTCTATAAA 1590
QY 1441 ATTGGATTTAGCGCTAAATATATATATACAGGTGCAATTAGGATGGACACACAGTAGTGT 1500
DB 1591 ATTGGATTTAGCGCTAAATATATATATATACAGGTGCAATTAGGATGGACACACAGTAGTGT 1650
QY 1501 AATAGAAATTAATGCAATATCAGATATAAATAATTAATCAATGATCCGCAAAATCAAGGTAAAC 1560
DB 1651 AATAGAAATTAATGCAATATCAGATATAAATAATTAATCAATGATCCGCAAAATCAAGGTAAAC 1710
QY 1561 AGCTTTGATACAACTCTAAGGTAAATTTGAAGGACCTGCTCATACAGGAGGAAACCTTGCT 1620
DB 1711 AGCTTTGATACAACTCTAAGGTAAATTTGAAGGACCTGCTCATACAGGAGGAAACCTTGCT 1770
QY 1621 TATTTACAAAGTCAAGGGCGTTTAGAGATTTACATGTAGAACTCTCTAATTTCTACACAATCT 1680
DB 1771 TATTTACAAAGTCAAGGGCGTTTAGAGATTTACATGTAGAACTCTCTAATTTCTACACAATCT 1830
QY 1681 TATTTACAAAGTCAAGGGCGTTTAGAGATTTACATGTAGAACTCTCTAATTTCTACACAATCT 1740
DB 1831 TATTTACAAAGTCAAGGGCGTTTAGAGATTTACATGTAGAACTCTCTAATTTCTACACAATCT 1890
QY 1741 CTTTCAATACAGGAGTAATAGGAATACCACTCAACGACTCAACACACACTTTTCTTGCT 1800
DB 1891 CTTTCAATACAGGAGTAATAGGAATACCACTCAACGACTCAACACACACTTTTCTTGCT 1950
QY 1801 ACAATTTATATAATTTTCAATACGAGATTTTGGGTATTTTCCAAATTTTCCAAAGTACAGTA 1860
DB 1951 ACAATTTATATAATTTTCAATACGAGATTTTGGGTATTTTCCAAATTTTCCAAAGTACAGTA 2010
QY 1861 ACATTTACCTTTTAAATTCGAAACATACCAATTTATATTTAATTCGTGAGATGATCAAAATTTCA 1920
DB 2011 ACATTTACCTTTTAAATTCGAAACATACCAATTTATATTTAATTCGTGAGATGATCAAAATTTCA 2070
QY 1921 ATTTTATCATTTGATATAAATTTGAATTTTATACCAATTTACTCTCTGTACGCCAAATATAGA 1980
DB 2071 ATTTTATCATTTGATATAAATTTGAATTTTATACCAATTTACTCTCTGTACGCCAAATATAGA 2130
QY 1981 GAAAAACAAAAATTTAGAACTATCCAAACAAAAATAAATACATTTTTCACAAATCATACA 2040
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Db      2131 GAAAAACAAAATTTAGAACTATCCAAACAAAATAAATACATTTTTCACAAATCATACA 2190
Qy      2041 AAAAAATCTTTAAATATAGAAAGCCACAAACTATGATATTTGATTA 2085
Db      2191 AAAAAATCTTTAAATATAGAAAGCCACAAACTATGATATTTGATTA 2235

RESULT 3
US-10-783-417-1
; Sequence 1, Application US/10783417
; Publication No. US20040216186A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-006, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274146
; CURRENT APPLICATION NUMBER: US/10/783,417
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,806
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2208)
US-10-783-417-1

Query Match      86.1%; Score 1794.4; DB 8; Length 2208;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1908; Conservative 0; Mismatches 141; Indels 9; Gaps 2;

Qy      1  ATGTGTCAAGGGGAATACAAATATGTGTGATAATTCGAGACATTTTCTAGTGTCTGATACA 60
Db      154  ATGTGTCAAGGGGAATACAAATATGTGTGATAATTCGAGACATTTTCTAGTGTCTGATACA 213
Qy      61  ATTGTGTCAGTTAGTCAGGTACTATTGTATCGGTACTCTGTAGCCGGTATAGGTGG 120
Db      214  ATTGTGTCAGTTAGTCAGGTACTATTGTATCGGTACTCTGTAGCCGGTATAGGTGG 273
Qy      121  CTCACCTTCTATATCCGGACCGATAGGAATAATAGGTGCTATAATAATATCTTTTGTACC 180
Db      274  CTCACCTTCTATATCCGGACCGATAGGAATAATAGGTGCTATAATAATATCTTTTGTACC 333
Qy      181  CTAATCACTGTCTTTTGGCCGGGAGAACAAAGACAAACAGTATGGACACAAATTTATT 240
Db      334  CTAATCACTGTCTTTTGGCCGGGAGAACAAAGACAAACAGTATGGACACAAATTTATT 393
Qy      241  AAAATGGGAGAAATTTTGTGTGATACACCGTTTAAACAGAAAGCATAAAAAGCTTAAAGTTA 300
Db      394  AAAATGGGAGAAATTTTGTGTGATACACCGTTTAAACAGAAAGCATAAAAAGCTTAAAGTTA 453
Qy      301  CAAACTTTTAGAGGATTTAGACAAATATTTACAAAGCTATAATACAGCATTAGATGATGG 360
Db      454  CAAACTTTTAGAGGATTTAGACAAATATTTACAAAGCTATAATACAGCATTAGATGATGG 513
Qy      361  AGAAAAATTTAAAGACTTACAACTCTCGATTACCACTCATCATCAGCATTTACAAAGCT 420
Db      514  AGAAAAATTTAAAGACTTACAACTCTCGATTACCACTCATCATCAGCATTTACAAAGCT 573
Qy      421  GCCTTGACTCTTAAAAATACGAATTTGAGAATGTTTCACAATGATTTTATTCGAGAAATACCT 480
Db      574  GCCTTGACTCTTAAAAATACGAATTTGAGAATGTTTCACAATGATTTTATTCGAGAAATACCT 633
Qy      481  GGTTCCTCAACTTGAACCTTATAAAACGCTATTACTACCTATTATTATGCGCAAGCTGCTAAT 540
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Db      634  GGTTCCTCAACTTGAACCTTATAAAACGCTATTACTACCTATTATTATGCGCAAGCTGCTAAT 693
Qy      541  TTTCAATTTAAATTTTATACAAACAGGTGCTGAATTTGGCTGATGAATGGAATGCAGATATA 600
Db      694  TTTCAATTTAAATTTTATACAAACAGGTGCTGAATTTGGCTGATGAATGGAATGCAGATATA 753
Qy      601  CATCTCTCAAAATTTGAACCTTAATGCTGGAAACATCAGATGACTATTATTAACTTTTAAAA 660
Db      754  CATCTCTCAAAATTTGAACCTTAATGCTGGAAACATCAGATGACTATTATTAACTTTTAAAA 813
Qy      661  GAAAAATATACCTTAAATATAGTAACTATTGTGCAAAATACCTATAGAGAAAGGACTTAAATAA 720
Db      814  GAAAAATATACCTTAAATATAGTAACTATTGTGCAAAATACCTATAGAGAAAGGACTTAAATAA 873
Qy      721  CTTGAAACGAAACCTTAATATGAGATGGAGTATATTATTAATGATTATTCGAAGATATATGACT 780
Db      874  CTTAGAGAGCAACCAATATGAAATGGAGTATATTATTAATGACTATTCGAAGATATATGACC 933
Qy      781  ATTACTGTATTAGATACTATCGCTCAATTTCTTTTATGATATAAAGAGATACAAGAT 840
Db      934  ATTACTGTATTAGATACCATCTCTCAATTTCTTTTATGATATAAAGAGATATAGAGAT 993
Qy      841  TCAATAGGAAGAATAG-----GTGGCATTAAAACTGAACTTACAAGAGAAAAATTTATACA 894
Db      994  TCAATAGGAAGAATAGAAAGCAATTAAGATGAACCTCAAGAGAAATTTATACA 1053
Qy      895  ACTGAAATAAAATTTTGGCGGTCTTACTTACCTTGAATTCACCCCAATCTCGCTATAATG 954
Db      1054  ACTGAAATAAAATTTTGGCGGTCTTCTCTCACTTAGAGTTCAACCCCAATCTAGCTAGCATG 1113
Qy      955  GAATATAATTTAAACAGTTTCAGGGCTTAGATTATTTTCATTTTATGATGAACTTATATT 1014
Db      1114  GAATATAATTTAAACAGTTTCAGGGCTTAGATTATTTTCAATTTTATGAGAACTTATTTT 1173
Qy      1015  TATACAAAAAATGAAACGTTACGGGAATCGTTAGTTGGTATTGCGAATCGTAAATAGATCT 1074
Db      1174  TATACAGAAATACAAATTCGGGAATCGTTAGTTGGTATTGCTAATCGTATGACCT 1233
Qy      1075  ACTTATGCTACGACAGGAACCTGAAATTTATATGAGAGAAAGAACAGGTCCACCCACAACA 1134
Db      1234  ACTTATGCAATFACTATAACTGAAACTTTATATGAGAGAAAGAACAGGTTCACCCACAACA 1293
Qy      1135  AAAACTTTAATACCAATTTGAATCCTATAAGTTTCAATTTGTAACCTGATAGACAAGTAAT 1194
Db      1294  AAAACAATAAGACCAATTTGAATCTTATAAGTTTCAATTTGTAACCTGATAGACAATCACCT 1353
Qy      1195  CCTACTTCCCTTTTCTTAAACATATACTTTTCAAAATTAATCAAAATGAACTTTTATTTAAAT 1254
Db      1354  CCTGTTTCCCTATTTC---AACCACACTTTAATTAATCAAAATGAACTTTTATTTAAT 1410
Qy      1255  AATTCACTCTAGTAAATTAACATATTACAGCTGGGGGAATTTATCTAATGATAAAAAA 1314
Db      1411  GGCCTCATCTAACACACACTCAAAATTTACAGCAGGAGGGTCTTTATCTAATATCAAAAC 1470
Qy      1315  ACAACTGATTTTCAATTTCTGTAAAAAGAGCTGTAAACCAATTTATTAATCCAAATTCCT 1374
Db      1471  ACAACTTTTCTTCAATTTCTGTAAAAAGAGCTGCAATCTAGTTATTGATCCAGGTGT 1530
Qy      1375  TTACCAAGCTATAATAGTTTATAGTCATATTTTATCCAGTTTCTTTTATTTAATTTATTC 1434
Db      1531  TCACCAAACTTTAATTAATAGTATAGTCATATTTTATCCCATTTTTCATTTTACTTATTC 1590
Qy      1435  TATAAAATTTGATTAGCGCTAAATATATATATACAGGTGCAATTAGGTGGACACACAGT 1494
Db      1591  TATGTGATTTGGATTACAGCTACAAATATTAGATAACAGGTGTATTAGGTGGACACACAGT 1650
Qy      1495  AGTGTTAATAGAAATTAATGCAATATCAGATAAAATTAATACATGATGATCCAGCAATCAA 1554
Db      1651  AGTGTGTAGATATAAATGCAATATCAGATAAAATTAATTAATGATGATCCAGCAATCAA 1710
Qy      1555  GGTAAACAGTCTTGTATACAACTCTAAGGTAAATTTGAAGGACCTGGTGGTCATACAGAGGAAAC 1614
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Db 1711 GGTAACAATCTTGATACAAACTCTAAGTAATTTGAAGGACCTGGTCATACAGGAGAAAC 1770
Qy 1615 TTGGTTTATTACAAAGCTCAAGGCGTTTGAAGATTACATGTAGAACTCTCTAATCTTACA 1674
Db 1771 TTGGTTTATTACAAAGCTCAAGGCGTTTGAAGATTACATGTAGAACTCTCTAATCTTACA 1830
Qy 1675 CAATCTTATTACATAGACTCGATACGCTACAAATGGTCTGGAATATCTTCTCTAAT 1734
Db 1831 CAATCTTATTTCATAGACTTCGATATGCTACAAATGGTCTGGAATATCTTCTCTAAT 1890
Qy 1735 ATATCTCTTCAATACACAGAGTAAATAGGAATACCACTCAACGACTCAACACACTTTT 1794
Db 1891 ATATCTCTTCAATACACAGAGTAAATAGGAATACCACTCAACGACTCAACACACTTTT 1950
Qy 1795 TCTGGTCAAAATTATAAATTTAACAATACGAGATTTTGGGTATTTTCCAAATTTCCAAAT 1854
Db 1951 TCTGGTCAAAATTATAAATTTAACAATACGAGATTTTGGGTATTTTCCAAATTTCCAAAT 2010
Qy 1855 ACAGTAACATTTACCTTTAAATCGAAACATACCACTTTATATTTAATCGTGAGATGTATCA 1914
Db 2011 ACAGTAACATTTACCTTTAAATCGAAACATACCACTTTATATTTAATCGTGAGATGTATCA 2070
Qy 1915 AATTCAATTTTAAATCATTTGATAAATTTGAATTTATACCAATTTCTCTCTGTACGCCAA 1974
Db 2071 AATTCAATTTTAAATCATTTGATAAATTTGAATTTATACCAATTTCTCTCTGTACGCCAA 2130
Qy 1975 AATAGAGAAACAAAAATTAGAAACTATCCAAACAAAAATAAATAAATTTTCCAAAT 2034
Db 2131 AATAGAGAAACAAAAATTAGAAACTATCCAAACAAAAATAAATAAATTTTCCAAAT 2190
Qy 2035 CATACAAAAATACCTTTA 2052
Db 2191 CATACAAAAACACTTTGA 2208

RESULT 4
US-09-756-526A-3
; Sequence 3, Application US/09756526A
; Patent No. US20020038005A1
; GENERAL INFORMATION:
; APPLICANT: Jana, Wojciechowska
; APPLICANT: Evgeny, Lewitin
; APPLICANT: Ludmila, Revina
; APPLICANT: Igor, Zalunin
; APPLICANT: Galina, Chestukhina
; TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
; FILE REFERENCE: S-30913A
; CURRENT APPLICATION NUMBER: US/09/756.526A
; PRIOR FILING DATE: 2001-01-08
; PRIOR FILING DATE: 2000-01-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4896
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(4896)
; OTHER INFORMATION: Bacillus thuringiensis supsp. finitimus strain VKPM B-1161 (taxon
; OTHER INFORMATION: :29337
; NAME/KEY: CDS
; LOCATION: (1129)..(4458)
; OTHER INFORMATION: product: Cry28Aa1 delta-endotoxin
; PUBLICATION INFORMATION:
; AUTHORS: Wojciechowska, et al.
; TITLE: Two novel delta-endotoxin gene families cry26 and cry28 from Bacillus
; TITLE: thuringiensis ssp. finitimus
; JOURNAL: FEBS Lett.
; VOLUME: 453
; ISSUE: 12
; PAGES: 46-48

; DATE: 1999-06-18
; DATABASE ENTRY DATE: ---
US-09-756-526A-3
Query Match 7.7%; Score 161.2; DB 3; Length 4896;
Best Local Similarity 57.0%; Pred. No. 3.3e-19;
Matches 385; Conservative 0; Mismatches 243; Indels 48; Gaps 3;
Qy 153 AGTGCTATTAATATCTTTTGGTACCTTAATCAGCTGTCTTTTGGCCCGGGGAGAAACA 212
Db 1293 AGTGCTATTAATATCTTTTGGTACCTTAATCAGCTGTCTTTTGGCCCGGGGAGAAACA 1352
Qy 213 AGA---CAAAACAGTATGACACAAATTTATTAATAATGGGAGAAATTTTGTGTATACACC 269
Db 1353 AGATCCAAAAAATTTGGTCAAAATTTATGAACACGAGAGAGACCTTTTAAATCAAAAC 1412
Qy 270 GTTAACAGAAAGCATAAAAAGCTAAAGTTTACAACTTTTAGAAGGATTTAGACAAATATT 329
Db 1413 AATTTCTACAGCTGTAAAGAAATAGCATTAAGCTCATCTAAATGGTTTAAAGATGTATT 1472
Qy 330 ACAAAGCTATAATACAGCATTTAGATGATTCGAGAAATTTAAAGAGACTTACAAAGCTCTGG 389
Db 1473 AAGTACTATGAAGAGCATTTAATGATTCGAGAGAAATCCAAAGTCAATATCTGCAG 1532
Qy 390 ATTACCAACCATCATCAGCATTTACAAACAGCTGCCTTGACTCTTTAAATAATACGATTTGAGAA 449
Db 1533 ATTGGTATCAGAA-----GATTTGAAAA 1556
Qy 450 TGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAATCTTATAAAACGCT 509
Db 1557 CGCTCAATTTTGTAAAGCAATATGCCAACCTCCAACTTCCCGATGACACATT 1616
Qy 510 ATTACTACCTATTATTCGCGAAGCTGTCTAATTTTCATTTAAATTTTATACAAAGGTGC 569
Db 1617 ATTATTAAGTTGCTATACAGAAAGCTGCAAAATTTATCAATTTGAATTTTATACATCAAGGTGT 1676
Qy 570 TGAATTCGCTGATGAATGGAATGAGATATACATATCTTTCAAAATGGAACCTAATATGCTGG 629
Db 1677 ACAATTCGCGATCAATGGATTCAGATCAACACATTCACCAAT-----GTTGAA 1727
Qy 630 AACATCAGATGATTTATTAATTAATCTTTTAAAGAAAAATATACCTAAATATAGTAACTATTG 689
Db 1728 GTCATCAGGTACTTATTATGACGAGCTATTGGTATATATTTGAAAAGTATATTAATATTG 1787
Qy 690 TGCAAAATACCTATAGAGAGGACTTAATAAATCTTGAACGAACTAATATAGATGAGAG 749
Db 1788 CACCAAGACATACCATAAAGGATTTGAATCACCCTTAAAGAAATCAGAAAAAATCATATGGA 1847
Qy 750 TATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATATCTATCGCTCAATT 809
Db 1848 TGCTTATACACATATGTCGAGAAATGACCTTAATTTGATTTGGATCTTTGCGCAACTTT 1907
Qy 810 TTCTTTTATGATATA 825
Db 1908 TCCTTTTTATGATATA 1923

RESULT 5
US-10-345-020-3
; Sequence 3, Application US/10345020
; Publication No. US20030150018A1
; GENERAL INFORMATION:
; APPLICANT: Jana, Wojciechowska
; APPLICANT: Evgeny, Lewitin
; APPLICANT: Ludmila, Revina
; APPLICANT: Igor, Zalunin
; APPLICANT: Galina, Chestukhina
; TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
; FILE REFERENCE: S-30913B
; CURRENT APPLICATION NUMBER: US/10/345.020
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/175,158
; PRIOR FILING DATE: 2000-01-07

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/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 3
/ LENGTH: 4896
/ TYPE: DNA
/ ORGANISM: Bacillus thuringiensis
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1129)..(4458)
/ OTHER INFORMATION: product: Cry28Aa1 delta-endotoxin
/ PUBLICATION INFORMATION:
/ AUTHORS: Wojciechowska, et al.
/ TITLE: Two novel delta-endotoxin gene families cry26 and cry28 from Bacillus
/ TITLE: thuringiensis spp. finitimus
/ JOURNAL: FEBS Lett.
/ VOLUME: 453
/ ISSUE: 12
/ PAGES: 46-48
/ DATE: 1999-06-18
/ US-10-345-020-3

Query Match          7.7%; Score 161.2; DB 6; Length 4896;
Best Local Similarity 57.0%; Pred. No. 3.3e-19;
Matches 395; Conservative 0; Mismatches 243; Indels 48; Gaps 3;

QY 153 AGTGTCTATAATAATATCTTTTGGTACCCTAATCACTGTCTTTTGGCCCGGGGAGAAC 212
DB 1293 AGGTGGTGACTTATATCATTTTGGAACTTGGCTCCCGTCTTTGGCCTGTATCCAGAG 1352

QY 213 AGA---CAAAACAGTAGTGACAAATTTTAAATGGGAGAAATTTTGTGTGATACACC 269
DB 1353 AGATCCAAAAAATTTTGGTCAAAATTTATGAAACACGAGAAAGACCTTTTAAATCAAC 1412

QY 270 GTTAAACAGAAACATATAAAGCTTAAAGTTACAAACTTTTAGAAGGATTTTAGACAAATATT 329
DB 1413 AATTCTACAGCTGTAAAGAAATAGCATAGCTCATCTAATGGTTTAAAGATGTATT 1472

QY 330 ACAAAGCTATAATACAGCATTTAGATGATGGAGAAAAATTTAAAGAACTACAAGCTCCTGG 389
DB 1473 AACGTACTATGAAGAGCATTTAATGATTTGGAAGAGAAAAATCCAAGTGCAATACTGCCAG 1532

QY 213 AGA---CAAAACAGTAGTGACAAATTTTAAATGGGAGAAATTTTGTGTGATACACC 269
DB 1353 AGATCCAAAAAATTTTGGTCAAAATTTATGAAACACGAGAAAGACCTTTTAAATCAAC 1412

QY 270 GTTAAACAGAAACATATAAAGCTTAAAGTTACAAACTTTTAGAAGGATTTTAGACAAATATT 329
DB 1413 AATTCTACAGCTGTAAAGAAATAGCATAGCTCATCTAATGGTTTAAAGATGTATT 1472

QY 330 ACAAAGCTATAATACAGCATTTAGATGATGGAGAAAAATTTAAAGAACTACAAGCTCCTGG 389
DB 1473 AACGTACTATGAAGAGCATTTAATGATTTGGAAGAGAAAAATCCAAGTGCAATACTGCCAG 1532

QY 390 ATTACCAACATCATCAGCATTTACAACAAGCTGCCTTGACTCTTTAAATACGATTTGAGAA 449
DB 1533 ATTGGTATCACAGA-----GATTTGAAAA 1556

QY 450 TGTTCACATGATTTTATTTCGAGAAATACCTGGTTTCCAACCTTTGAAACTTATAAAACGCT 509
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QY 810 TTCCTTTTATGATATA 825
DB 1908 TCCTTTTATGATATA 1923

RESULT 6
US-10-342-821-3
/ Sequence 3, Application US/10342821
/ Publication No. US20030154510A1
/ GENERAL INFORMATION:
/ APPLICANT: Jana, Wojciechowska
/ APPLICANT: Evgeny, Lewitin
/ APPLICANT: Ludmila, Revina
/ APPLICANT: Igor, Zalunin
/ APPLICANT: Galina, Chestukhina
/ TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
/ FILE REFERENCE: S-30913C
/ CURRENT APPLICATION NUMBER: US/10/342,821
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/175,158
/ PRIOR FILING DATE: 2000-01-07
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 3
/ LENGTH: 4896
/ TYPE: DNA
/ ORGANISM: Bacillus thuringiensis
/ FEATURE:
/ NAME/KEY: source
/ LOCATION: (1)..(4896)
/ OTHER INFORMATION: Bacillus thuringiensis supsp. finitimus strain VKPM B-1161 (taxon
/ OTHER INFORMATION: :29337
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1129)..(4458)
/ OTHER INFORMATION: product: Cry28Aa1 delta-endotoxin
/ PUBLICATION INFORMATION:
/ AUTHORS: Wojciechowska, et al.
/ TITLE: Two novel delta-endotoxin gene families cry26 and cry28 from Bacillus
/ TITLE: thuringiensis spp. finitimus
/ JOURNAL: FEBS Lett.
/ VOLUME: 453
/ ISSUE: 12
/ PAGES: 46-48
/ DATE: 1999-06-18
/ US-10-342-821-3

Query Match          7.7%; Score 161.2; DB 6; Length 4896;
Best Local Similarity 57.0%; Pred. No. 3.3e-19;
Matches 395; Conservative 0; Mismatches 243; Indels 48; Gaps 3;

QY 153 AGTGTCTATAATAATATCTTTTGGTACCCTAATCACTGTCTTTTGGCCCGGGGAGAAC 212
DB 1293 AGGTGGTGACTTATATCATTTTGGAACTTGGCTCCCGTCTTTGGCCTGTATCCAGAG 1352

QY 213 AGA---CAAAACAGTAGTGACAAATTTTAAATGGGAGAAATTTTGTGTGATACACC 269
DB 1353 AGATCCAAAAAATTTTGGTCAAAATTTATGAAACACGAGAAAGACCTTTTAAATCAAC 1412

QY 270 GTTAAACAGAAACATATAAAGCTTAAAGTTACAAACTTTTAGAAGGATTTTAGACAAATATT 329
DB 1413 AATTCTACAGCTGTAAAGAAATAGCATAGCTCATCTAATGGTTTAAAGATGTATT 1472

QY 330 ACAAAGCTATAATACAGCATTTAGATGATGGAGAAAAATTTAAAGAACTACAAGCTCCTGG 389
DB 1473 AACGTACTATGAAGAGCATTTAATGATTTGGAAGAGAAAAATCCAAGTGCAATACTGCCAG 1532

QY 390 ATTACCAACATCATCAGCATTTACAACAAGCTGCCTTGACTCTTTAAATACGATTTGAGAA 449
DB 1533 ATTGGTATCACAGA-----GATTTGAAAA 1556

QY 450 TGTTCACATGATTTTATTTCGAGAAATACCTGGTTTCCAACCTTTGAAACTTATAAAACGCT 509
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Db 1557 CGCTCAATTCAAATTTTGTAAAGCAATATGCCCAACTCCCACTCCCAAGTATGACCAAT 1616
Qy 510 ATTACTACCTATTTATGCGCAAGCTGCTAAATTTTCAATTTTAAATTTTATACAAAGGTGC 569
Db 1617 ATTATTAAGTTGCTATACAGAGCTGCAAAATTTTACATTTTGAAATTTTATACATCAAGGTGT 1676
Qy 570 TGAATTTGGCTGATGAATGGAAATGAGATATACATCTTTCACAAATTTGAACTAATGCTGG 629
Db 1677 ACAATTTGGCGGATCAATGGAAATGAGATCAACCAATTCACCAAT-----GTTGAA 1727
Qy 630 AACATCAGATGACTATTTATAAACTTTTAAAGAAATATACCTAAATATAGTAATG 689
Db 1728 GTCATCAGGCTACTTATTTATGACGAGCTTTGGTATATTTTGAAGAATGATTAATTTATG 1787
Qy 690 TGCAAAATPACCTATAGAGAGGACTTAAATAAACTTTGAAACGAACCTAATATGAGATGGAG 749
Db 1788 CACCAAGACATACCATAAAGGATTTGAATCACCTTAAAGAATCAGAAAAAATCAATGGGA 1847
Qy 750 TATATTTAATGATTTATCGAAGATATGACTATTTACTGTATTAGATACTATCGCTCAAT 809
Db 1848 TGCTTATAACACATATCGTCGAGAAATGACCTTAATTTGTTATGGATCTTGTGCGCAACTTT 1907
Qy 810 TTCTTTTATGATATA 825
Db 1908 TCCTTTTATGATATA 1923

RESULT 7
US-10-311-455-2128/c
; Sequence 2128, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; FILE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311.455
; PRIOR FILING DATE: 2002-12-16
; PRIOR FILING DATE: 2001-07-02
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 2128
; LENGTH: 15548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2128

Query Match 5.6%; Score 117; DB 6; Length 15548;
Best Local Similarity 43.6%; Pred. No. 6.2e-11;
Matches 819; Conservative 0; Mismatches 1040; Indels 18; Gaps 6;

Qy 218 AAACAGTATGACACAAATTTTAAATGGGAGAAATTTTGTGATACACCGTTAACAG 277
Db 13398 ATAAATATACACGCATATAATATATACGTATAAAATATATATATAATATAATATACACGT 13339
Qy 278 AAGCATAAACAGCTAAAGTTACAACTTTTAGAAGGATTTAGACAAATATTTACAAAGCT 337
Db 13338 CTAATATATATATATATAATATAATTTTACGTATAAAATATATATCTCTAAATATATATAT 13279
Qy 338 ATAATACAGCATTTAGATGATTTGGAGAAATTTAAAGAACTACAGCTCTCGGATPACCAC 397
Db 13278 AAATATATATCTAAATATATATATAAAATATATATCTAAATATATATATAATATAAATA 13219
Qy 398 CATCATCAGCATTAACAAGCTGCTTGACTTTTAAATACGATTTTGAGATGTTTCA 457
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Db 13218 TATATCTAAATATATATATAATATAATATCTAAATATATATATAATATAATATAATATATC 13159
Qy 458 ATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTATAAAACGCTTACTACTAC 517
Db 13158 TAAATATATATATATAATATAATATAATCTAAATATATATATAATATAATATAATATAATAA 13099
Qy 518 CTATTTATGCGCAAGCTGCTAAATTTTCATTTAAATTTTATTACAAAGGTGCTGGAATGG 577
Db 13098 ATATATATATATAA---AATATATATAAATATATATATAAATATATATAATATAATAA 13042
Qy 578 CTGATGAATGAATGAGATATACATCTTTCACAAATTTGAACCTTAATGCTGGACATCAG 637
Db 13041 TACATATATAAATATATATATAATATAATATAATATAAATATATAATATAATATAATATAA 12983
Qy 638 ATGACTTATATAAATTTTAAAGAAATATACCTAAATATAGTAATCTTTTGTGCAATA 697
Db 12982 ATATAAATATATATAAATATATATAAATATATATAAATATATATAATATAATATAATATA 12923
Qy 698 CCTATAGAGAGGACTAAATATAAATTTGAAACGAACCTAATATGAGATGGAGTATATTA 757
Db 12922 TATATATACGAATATATATAATATAATATAATATAATATAATATAATATAATATAATATA 12863
Qy 758 ATGATTTATCGAAGATATGACTATTTACTGTATTTAGATACATTCGCTCAATTTTCTTTT 817
Db 12862 TAATATATATACGAAATATATATACGAAATATATAATATAATATAATATAATATAATATA 12803
Qy 818 ATGATATAAGAGATACAAAGATTCATAGGAAGATAGGTGGCATTTAAACCTCAACTTA 877
Db 12802 ACGAAATATATATACGAAATATATAATATAATATAATATAATATAATATAATATAATACG 12743
Qy 878 CAAGAGAAATTTTATACAACTGAAATAAATTTTGACCGCTTTTACTTACCTTGAAATTTCA 937
Db 12742 TATATATATAATATAATATAAATATAATATAATATAA---CGAAATATATAATATAATATA 12684
Qy 938 CCAATCTCGCTTAATGGAATATAATTTAAACAGCTTCAGGCTTAGATTAATTTTCATTTT 997
Db 12683 AAAATATATATACGAAATAAATATATAATATAATATAAATATAATATAATATAATACGAA 12624
Qy 998 TAGATGAACCT-TATATTTTATACAAAAAAGTAAACGCTGCGGAAATCGTTTGTAGTTGTT 1056
Db 12623 TATATAATATATATATAATATAAATATAATATAATATAATATAATATAATATAATATAA 12564
Qy 1057 GCGAATCGTAATAGATCTACTTATGCTACGACAGAACTGAAATTTATATATATATATAT 1116
Db 12563 TAAATATATATATAAATATAATATAATATAATATAATATAATATAATATAATATAATATAA 12504
Qy 1117 ACAGGTCACCCCAACAAACAACTTTA-----ATACCAATTTGAATCCTATAAAGTT 1167
Db 12503 ATATATATATAAATATATAATATAAATAATATAATATAAATAATATAATATAAATAATAT 12444
Qy 1168 TCAATTTGTAAGTATAGACAAAGTAACTTCTTACTTTCCCTTTTCCCTAACATATATCTTACA 1227
Db 12443 ATATATATAACATATATACATAAATAATATAATATAATATAATATAATATAATATAATAT 12384
Qy 1228 ATTAATCAAAATTTGAACCTTTTATTTAAATAATTTCACTAGTAATAAATTAACATATTTCA 1287
Db 12383 ATATAACATATATATATAATATAACATATATAATATAACATATATAATATAATATAATATA 12324
Qy 1288 GGGGGGAATTTATCTAATGATATAAATAAACAACACTGAATTTTCAATTTTCTGTTAAAAA 1347
Db 12323 AACATATATATATAACATATATAATAACATATATAATAACATATATAATATAATATAAACA 12264
Qy 1348 TGTAAACCAATTTAATTCAAATTTGTTTACCAAGCTATATAGTTTATAGTCATATTTTA 1407
Db 12263 TATATATAAATATAATATAAATATAATATAAATATAATATAAATATAATATAAATATAA 12204
Qy 1408 TCCAGTTTTCTTTATTTAA---TTATTCCTATAAATTTGGATTTAGCGCTAAATATATTA 1464
Db 12203 TATATAACATATATATAATATAATATAATATAATATAATATAATATAATATAATATAA 12144
Qy 1465 TATACAGGTGCAATTTAGGATGGACACACAGTAGTGTGTTAATAGAAATTAATGCAATATCAG 1524
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Db 1874 CAAGACCTAATAATAATACCTACAGATTTTAAATAATGAAGAGTTTAGATACAAAGATC 1933
Qy 1839 -TTTCCAAATTCAGTACAGTAACTACCTTTAAATCGAAACATACCAATTTATATTTA 1997
Db 1934 CTTTGTGATGCAATTTGTACCGATGAGATTTATCTTAACTAACTGATAAATATAGCTATTC 1993
Qy 1898 ATCGTGCAGATGT--ATCAAAATTCAAATTTAATCATTTGATGATAAAATTTGAATTTATACCA 1954
Db 1994 AACCATTAACATGACTTCCAATAATCACTGATGATTTAGCAGATCGAAATTTATCCAA 2053
Qy 1955 TTACTTCTCTGTCAGCGCAAAATAGAGAAAACAAAATTTAGAACTATCCAAACAAAA 2014
Db 2054 TCACTCAATCTGATTAGATGAGACAGAGAACCAAAATTTAGAAATCAGAACGAGAAGTTG 2113
Qy 2015 TAAATACATTTTTCACAAATCATACAAAATATCTTTAAATATAGAGCCACAACTATG 2074
Db 2114 TGAATGACTGTTTACAAATGACGCGAAAGATGATTTAAACATTTGGAACGACAGATTTATG 2173
Qy 2075 ATATTGATTAA 2085
Db 2174 ACATAGATCAA 2184

RESULT 9
US-10-312-841-1/c
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

Query Match 4.8%; Score 99.2; DB 6; Length 3673778;
Best Local Similarity 43.7%; Pred. No. 9.6e-07;
Matches 811; Conservative 0; Mismatches 1028; Indels 15; Gaps 8;

Qy 218 AACAGTATGGACACAATTTTAAATGGGAGAAAATTTTGTGTGATACACCGTTAACAG 277
Db 1715486 ATAAATATATACATATAAAATATATATATAAAATATACATATAAAATATATAAA 1715427

Qy 278 AACGATTAACACGTTAAAGTTACAACTTTAGAG-AGGATTTAGACAAATATTACAAAGC 336
Db 1715426 TATACATATAAAATATACATATAAAATATATATAAAATATACATATAAAATATATA 1715367

Qy 337 TATAATACAGCATTTAGATGATTTGGAGAAAATTTAAAGACACTACAGCTCTCGGATTTACCA 396
Db 1715366 TATAAAATATACATATAAAATATATATAAAATATATATAAAATATATAAAATATATA 1715307

Qy 397 CCATCATCAGCATTTACAAACAGCTGCTTGTAGCTCTTAAATATACGATTTGAGAAATGTTCCAC 456
Db 1715306 ATATATATAAAATATATATAAAATATATATAAAATATATATAAAATATATATAT 1715247

Qy 457 AATGATTTTATTCGAGAAATACCTGGTTTCCAACTTTGAACTTATAAAACGCTATTACTA 516
Db 1715246 ATAAATATATATAATAAAATATATATAAAATATATATAAAATATATATAATAAA 1715187

Qy 517 CCTATTTATGGCCA----AGCTGCTTAATTTTCATTTAAATTTTATTTACAAACAGGCTGGA 572
Db 1715186 TATATATATAAAATATATATAAAATATATATAAAATATATATAAAATATATATAAA 1715127
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Qy 573 ATTGGCTGATGAATGGAATGCAGATATACATCCTTCAAAATGAACTTAATCCTCGAAC 632
Db 1715126 TATAAAATATATATAAAATATATATAAAATATATATAAAATATATATAAAATATATA 1715067

Qy 633 ATCAGATGACTATTATAAACTTTTAAAGAAATATACCTTAAATATAGTAGTAATCTGTCG 692
Db 1715066 TAAAAATATATATAATAAAATATATATAAAATATATATAAAATATATATAAAATATATA 1715007

Qy 693 AAATACCTTATAGAGAAGGACTAAATAAACTTCGAAACGAAACCTTAATATGAGATGGAGTAT 752
Db 1715006 AAATATATATATATAAAATATATATAAAATATATATAAAATATATATAAAATATATA -TAT 1714948

Qy 753 ATTAAATGATTTATCGAAGATATATGACTATTACTGTATTAGATACATCTCGCTCAATTTTC 812
Db 1714947 ACAAATATATATATACAAATATATATAAAATATATATAAAATATATATAAAATATATA 1714888

Qy 813 TTTTATGATATAAAGAGATACAAAGATTCAAATAGGAAGATAGGTGGCACTTAAACTGA 872
Db 1714887 TATATATATAAAATATATATAAAATATATACATATAAAATATATATACTATATATAAA 1714828

Qy 873 ACTTACAAGAGAAATTTATACAACTGAAATATAAATTTTGACCGTCTTACTTACCTTGAAT 932
Db 1714827 ATATAAATATATATATAAAATATATATAAAATATATATAAAATATATATAAAATATA 1714768

Qy 933 TCAACCCAACTCTCGCTATATAATGGAATATAATTTAAACACGTTTCAGGGCTTATATTTTC 992
Db 1714767 TATACATATAAAATATATATAAAATATACATATAAAATATACATATAAAATATACATA 1714708

Qy 993 ATTTTATGACTTATATATTTTATACAAAATATGAACTGACCGGAATCGTTAGTTGG 1052
Db 1714707 TAAAAATATACATATAAAATATACATATAAAATATATATAAAATATATATA -TAAAAATATA 1714649

Qy 1053 TATTGCGAATCGTAATAGATCTACTTATGCTAGCAGAGAACTGAAATATATATATAGAGA 1112
Db 1714648 TATATAAAATATATATATAAAATATATAAAATATATATAAAATATATATAAAATATACA 1714589

Qy 1113 AAGAACAGGTCCACCCCAACAAACAAATTTTAAATACCAATTTGAATCTTATAAGTTTCAAT 1172
Db 1714588 TAAAAATATATATATAAAATATATACATATAAAATATATAAAATATATATAAAATATA 1714529

Qy 1173 ---TGTAACCTGATAGACAAGTAACTCTACTTCCCTTTTCCCTAACATATATTTACAT 1229
Db 1714528 ATATATAAAATATATAAAATATATATAAAATATATATAAAATATATATAAAATATA 1714469

Qy 1230 TAATCAAAATGAACTTTTATTTAAATTAATTCACCTAGTAATAAATAAATTAACATATTCAGCTGG 1289
Db 1714468 TATATAAAATATATATAAAATATATATAAAATATATATAAAATATATATAAAATATAT 1714409

Qy 1290 GGGGAATTTTATCTAATGATATAAAACAACTGATTTTCAATTTCTGTAAAAAAGACTG 1349
Db 1714408 ATATAAAATATATAAAATATATATAAAATATATATAAAATATATATAAAATATA 1714349

Qy 1350 TAAACCAATTTAATCCAAATTTGTTTACAGCTATAATAGTTATAGTCATATTTTATC 1409
Db 1714348 TATATATAAAATATATAAAATATATA -TAAAAATATATAAAATATATAAAATATATA 1714290

Qy 1410 CCAGTTTTCTTTATTTTATTTTCTCTATAAAATTTGGATTTAGCGCTAAATATATTATATAC 1469
Db 1714289 TATAAAATATATATAAAATATATAAAATATATAAAATATATAAAATATATAAAATATA 1714230

Qy 1470 AGGTGCATTTAGTAGGACACACAGTAGTGTGTTTAAATAGAAATTAATGCAATATCAGATAAAAT 1529
Db 1714229 TATATATAAAATATATATAAAATATATAAAATATATAAAATATATAAAATATATA 1714170

Qy 1530 AATTCAATGATCCAGCAATCAAAGGTAAACAGTCTTGATACAACTCTAAGGTAAATGA 1589
Db 1714169 AAAATATATATAAAATATATAAAATATATAAAATATATAAAATATATAAAATATATA 1714110

Qy 1590 AGGACCTGGTCATACAGGAGGAAACTTGTTTATTACAAAGTCAAGGCGCTTTAGAGAT 1649
Db 1714109 TAAATATATATAAAATATATATAAAATATATAAAATATATAAAATATATAAAATATAT 1714050

Qy 1650 TACATGTAGAACTCTTAATCTTACACATCTTTATTACATTAGACTTCGATACGCTA---C 1706
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Db	1714049	AAATATATATAAAATATATATATAAAATATATATAAAATATATATAAAATATATATA	1713990
Qy	1707	AAATGGTGTGGAAATACTCTTCTTAATATATCTTTACAATACCAGGAGTAATAGGAAT	1766
Db	1713989	AAATATATATATAAAATATATAAAATATATATAAAATATATAAAATATATATAT	1713930
Qy	1767	ACCACCTCAACGACTCAACAACTTTTTCTGTGACAAATTAATAAATTTACAATACGG	1826
Db	1713929	AAATATATATAAAATATATATAAAATATATAAAATATATATAAAATATATAAAATATAT	1713870
Qy	1827	AGATTTTGGGTATTTCCAAATTTCCAAAGTACAGTAACAATTTACCTTTAAATCGAAACATACC	1886
Db	1713869	ATATAAAATATATATAATATATATAAAATATATAAAATATATAAAATATATAAAATATATAA	1713810
Qy	1887	ATTATATATTTAAATCGTGCAGATGTATCAAAATTTCAATTTTAAATCAATTCGATAAAATTCGAAT	1946
Db	1713809	ATATATATAAAATATATAAAATATATAAAATATATAAAATATATAAAATATATAAAATATATAA	1713750
Qy	1947	TATACCAATTTACTCTCTGTACGCCAAATATAGAGAAAAACAAAAATTTAGAAACTATCCA	2006
Db	1713749	ATATATATATAATATATATAATATATAATATATATATATATATATAATATAAAATATATA	1713690
Qy	2007	ACAAAAATATAACATATTTTCAAAATCATACAAAAATCTTTTAAATATAGA 2060	
Db	1713689	TA-AAATATATATAAAATATATAAAATATATAAAATATATAAAATATATAAAATATATA 1713637	
RESULT 10			
US-10-473-126-386/c			
; Sequence 386, Application US/10473126			
; Publication No. US20040234973A1			
; GENERAL INFORMATION:			
; APPLICANT: Epigenomics AG			
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell			
; FILE REFERENCE:			
; CURRENT APPLICATION NUMBER: US/10/473,126			
; CURRENT FILING DATE: 2003-09-26			
; NUMBER OF SEQ ID NOS: 1258			
; SEQ ID NO 386			
; LENGTH: 8056			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)			
US-10-473-126-386			
Query Match 4.5%; Score 93.6; DB 8; Length 8056;			
Best Local Similarity 43.4%; Pred. No. 9e-07;			
Matches 847; Conservative 0; Mismatches 1079; Indels 26; Gaps 8;			
Qy	147	AATAATAGGTGCTATAATAATATCTTTTGTACCTTAATCACCTGCTTTGGCCCGCGG	206
Db	7433	AATAACATATATATATATACATATTTTTTTTTTCCAAATATTTTTTTTTTAAAAATA	7374
Qy	207	AGAACAGACAAACAGTAGTAGGACACAATTTATTAATAATGGGAGAAATTTTTGTGTAC	266
Db	7373	ATAAAAAAATAAAAAATTTATTTAAATATTTTTTAAATAAAAAATTTAAAAATAAAAAA	7314
Qy	267	ACGGTTAACGAAAGCATAAACAGCTAAAGTTACAACTTTAGAGAGATTAGACAAAT	326
Db	7313	ATATTTTTTTTATATATCATATAAAATATATAAAATATAAAATTTCAAAAAATATAT	7254
Qy	327	ATTACAAAGCTATAATACAGCATTTAGATGTTGGAGAAATTTAAAGACTACAAGCTCC	386
Db	7253	ATTATATATTAAATATAAATTTTAAAAATAAATAATATATATAAATAATTAATAA	7194
Qy	387	TGGATTACCAAC-CATCATCAGCATTTACAACGCTCGCTTGACTCTTAAAAATACGATTTG	445
Db	7193	TTAATTAAATCAAAACATAAATAAATAAATAAATATACATTTACAAATTTATATAATA	7134
Qy	446	AGNATGTTCAATGATTTTATTCGAGAAATACCTGGTTCCAACTTGAACTTATAAAA	505

Db	7133	TTTTTATTAATATTTAAAAAAATTTATAAAATTTATAAAATTTAAAAATTTAATTTAAAAA	7074
Qy	506	CGCTATTACTACCTATTTATATGCGCAAGCTGCTAAATTTTTCATTTTAAATTTTATTAACAAG	565
Db	7073	ATAATTTAAATTTTAAATTTTAAAAATTTTTTTTTTTTTTAAAAAATAACAAAAATAAT	7014
Qy	566	GTGCTGAATGCTGCTGATGAATGCAATGCGAGATATACATCTCTTCACAAATTTGAACC--TAA	623
Db	7013	ATTTTTTTTTTTTTTTTTTAAATTTAAAAATCAATATATTTTTTTTATATATAATCATATTTTAA	6954
Qy	624	TGCTGGAACATCAGATGACTATTATATAAATCTTTTAAAAAGAAATATACCTTAAATATAGTAA	683
Db	6953	TAAATAAAAAAATAAAAAATTTTAAAAAATAAATTTAAACATTCATTTTTCAAAAAATAA	6894
Qy	684	CTATTGTGCAATACCTATPAGAGAGGACTAAATAAACTTCGAAAAAGAACCTTAATATGAG	743
Db	6893	AAAAATTAAACAAATTTTTTTTATAAAAAATTTTAAATTTTTCAAATTCAAATTTATAAAAT	6834
Qy	744	ATGGAGTATATTAAATGATTATCGAAGATATATGACTATTACTGTATTAGATACTATCGC	803
Db	6833	TTTTTATTTATTTTTTTTAAAAAAATTCAAATTTCCAAATTCAAATATTTTTTATTTTTTTTA	6774
Qy	804	TCAAATTTTCTTTTATGATATAAGAGATACAAAAGATTCAAATAGGAAAGAAATAGGTGGCAT	863
Db	6773	TATTTTTTCAATTAATTTTTTAAATTTTAAATTTCAATTAATTCAAAATTTATTATATAA	6714
Qy	864	TAAAACTGAACTTACAAGAGAAA-----TTTATACAACCTGAAATAAAATTTTGA 911	
Db	6713	TCAACATTATAAAACATAAAAAAATTTTATTTTTTTTAAAAATTTTAAATTTAAAAATTTAAA	6654
Qy	912	CGTCTTACTTACCTTGAAATTCACCCCAATCTCGTATAATGGAATATAATTTTACACG	971
Db	6653	ATTTCATATAAAAAACATAAAAAATAAAACAATAAATAATAAATAAATAAATAAATAA	6594
Qy	972	TTTCAGGGCTTACATTTATTTTTCATTTTATAGTCAACTTATATTTTATACAAAAAATGAAAC	1031
Db	6593	TTTTTTTTTCAATTTAAATTTTAAATTAATAAATAAATAATTTTAAATTTAAATTAAC	6534
Qy	1032	GTACGGGAATCGTTTAGTTGGTATTTCGGAATCGTAAATAGATCTACTTATGCTACGACAG	1091
Db	6533	ATTTTTCATACAAAATTTTACAAAAATTTTAAATAAACAATAAATAAATAAATAATTTAT	6474
Qy	1092	AACGAAATTTATATATGGGAAAGAACAGCTCCACCACCAACAACAACTTTTAA--TACCA	1149
Db	6473	TATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6414
Qy	1150	TTTGAATCCTATAAAAGTTTTCATTTGTAAGTATGACAGAGTAACCTCTACTTCCCTCTTT	1209
Db	6413	TATATATATAATATATATATATATATATTTTTTTTAAATAAATAAATAAATAAATAAATA	6354
Qy	1210	CCTAACATATACCTTTTCAATTAATCAAAATGAAGCTTTTATTTAAATAATTTTCACTAGTAAT	1269
Db	6353	ACACATTTTTTAAATATACATAATAATTAATTAATTAATTTTAAATTTTAAATTTTAAATAT	6294
Qy	1270	AAATTAACATATTACGCTGGGGGAA-TTTATCTAATGATAAATAAATAAATAAATAAATAA	1328
Db	6293	CAATTTTTTTTTTATATTTTTTATTTTTTATTTTATTTTAAATTTTAAATTTTACATTTTAA	6234
Qy	1329	ATTTCTCTGTAATAAAGAGCTGTAAACCAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA	1388
Db	6233	ACACATTTTATATATTAAATTTTAA	6174
Qy	1389	TAGTTATAGTCATATTTTATCCAGTTTCTTTTATTTTAAATTTTCTATATAAAT-TGGAT	1447
Db	6173	AATTTTTTTTTTAAATTTTAAACAAACATTTTATAAATTTTAAATTTTAAATTTTAAATTTTAA	6114
Qy	1448	TAGCGCTAAATATATATATACAGGTGCNTTAGGATGGACACACAGTAGTGTGTTAATAGMA	1507
Db	6113	AAACACATAATACATTTTCAATATAAATAAATAAATTTTCAATTTTCAATTTTCAATTTTATTT	6054
Qy	1508	ATAATGCAATATCAGATAAATAAATAATTTTCAATGATCCAGCAATCAAGGTGTAACAGCTTTG	1567

Db	6053	ATAAATAAA-----AAATACAAATTTATTAAATAATATTATTATTCAAAAAAAATAATAAAAAAA	5998
Qy	1568	ATACAAACTCTAGGTAAATTTGAAGGACCTCGTGCATACAGGAGGAAACTCTGGTTTATTATTC	1627
Db	5997	AAAAAAAAATTTAAAAAAAATTAATAAAATAATAAACACACATAATTAATTTTATACAA	5938
Qy	1628	AAAGTCAAGGCGTTTATAGAGATTACATGTAGAACTCTCTAAATCTACACAATCTTATACA	1687
Db	5937	TTTTTTTTTATTATTATATATTTTAAAAATTAATAATATTCAATTAATTCAAATTTTAAAA	5878
Qy	1688	TTAGACTTCGATAGCTACAAATGGTGGTGGAAATACCTCTCTCTTAATATATCTCTTACAA	1747
Db	5877	TTTTATTTTTTTTATTTTTTTTTTTTTTTTATATAAACATTTTTTTTTCAAAT---TTTTAAAA	5821
Qy	1748	TACCAGGAGTAATAGGAATACCCTCAACGACCTCAACAACACCTTTTCTCGGTACAAAT	1807
Db	5820	TAAAAAACATAAAAAAAATAAAAAAAATTTTTTTTTCATTAAATTTTCATTATCAATTTT	5761
Qy	1808	ATATAATATTTACAATACGGAGATTTTCGGTATTTTCCAAATTTTCCAGTACAGTAACTATC	1867
Db	5760	TTATAATACAAAAATTTTAAACAAATTAATAAAATTTTTTCAAAATTATATATTCCAAATCAT	5701
Qy	1868	CTTTAAATCGAAACATACCATTTATATTTAAATCGTGCAGATGTACAAATTCAAATTTTAA	1927
Db	5700	CATCAAAATTCAAATCAATTTTAAATTTTTTTTTTTTATATTTTCAAAAAAATAAAATTTTTTANA	5641
Qy	1928	TCATTGATAAAAATTTGAATTTTATACCAATTTACTTCTCTGTACGCCAAAAATAGAGAAAAAC	1987
Db	5640	AAATTTACAAAAAAAATAAAAAAATAAAAAAATTCATTAATATAAAATTCAAATTTTCAA	5581
Qy	1988	AAAAATAGAAACTATCAAAACAAAAATAAATACATTTTTTTCACAAATCATACAAAAATA	2047
Db	5580	AAATTTATTATTTTCAATTATTAATAATTTTAAATAAAATAAAAAAATAAAAAAACAACAACATC	5521
Qy	2048	CTTTAAATATAGAGCCCAAACTATGATATT	2079
Db	5520	AAATTAATAATAAAAAATCAAAACAAATAAAAAT	5489

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RESULT 11
US-10-473-126-240/c
; Sequence 240, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473.126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 240
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-240

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Query Match	4.2%	Score 86.8;	DB 8;	Length 8056;
Best Local Similarity	43.3%	Pred. No. 1.6e-05;		
Matches 727; Conservative	0;	Mismatches 933;	Indels 21;	Gaps 6;
QY	390	ATTACACCATCATCAGCATTTACAACAGCTGCCCTTGACTCTTAAAAATACGATTTGAA	449	
Db	1700	ATTTTATAAATTTTAAATAAAATATATTTATCGTATTAATAATAATTTTTTTTTTAA	1641	
QY	450	TGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAACGCT	509	
Db	1640	TTTTACGATTCGTTTATTTTCGATTTTTTAAAAATATTAATAATTATAAATAATAAAT	1581	
QY	510	ATTACTACCTATTTATGCGCAAGCTGCTAAATTTTCATTTAAATTTTATTAACAACAGGTGC	569	

1580	Db	ATTAATTTAAATATAATTTTAAAAAATAATTTTATTTTAAAAATTTTTTTTTTAAACGTAT	1521
570	Qy	TGAATTTGGCTGATGAAATGGAATGCAGATATACATCTTCACAAAATTGAACCTTAATCCTGG	629
1520	Db	TTATATTTTATATTTATATAAATAATTAATTTTAATAATTTTATTTTAAATATAATTTTAT	1462
630	Qy	AACATCAGATGACTATATTAABACTTTTAAAGGAAATATACCTTAAATATAGTAACATTG	689
1461	Db	TAAAAAATAATTTTATTTTATTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAA	1402
690	Qy	TGCAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACTTAATATAGATGGAG	749
1401	Db	CGATATTTTATTAATAAATAAATAAATTTTAAATAAATAAATAAATAAATAAATAAATAA	1342
750	Qy	TATATTTAATGATTTATCGAAGATATATGACTATCTGTAATTAGATACTATCCTCAATT	809
1341	Db	TTTTTAAAAAATTAATAATAAAATTTTAAAAATAATTTTAAATTTTAAAAAATAATACGT	1282
810	Qy	TTCTTTTATGATATAAAGGATACAAAGATTCAATAGGAAGAATAGTGGCAATTAAC	869
1281	Db	TTTTTATATATTAATAATAATTCGTAACTTTTTTTTATTCGAAATAATTTATTTTATAT	1222
870	Qy	TGAACCTACAAGAGAAATTTTACAACCTGAAATAAAATTTTGACCGCTTACTTACCTTGA	929
1221	Db	TAAAAAATAATTAATAATAATTTTAAAAATTTTAAATAAATAATTAATAAATCGAAAA	1162
930	Qy	AATTCACCAACTCTCGCTATAATGGAATATAATTTAAACAGCTTCAGGGCTTAGATTATT	989
1161	Db	TATTAATTTTAAATTTTCGAATATCGAAAAATAATTTAAAAAACAATAATAAACGTTTT	1102
990	Qy	TTCAATTTTATGATGAACCTTATTTTATACAAAAATGAAACGTACGGGAATCGTTTGT	1049
1101	Db	AAAAACGTTAAAAAATAAACAAGATTTAAACGAAATTTTTTTTATTCGTAATAATTTTC	1042
1050	Qy	TGTTATTCGCAATCGTAATAGATCTACTTATGCTACGACAGAACTGAAATTTAT-ATAT	1108
1041	Db	GAAATTAATAAATAAATAAATAATTTTAAATAATTTTAAAAAATAATTAATAATA	982
1109	Qy	GAGAAAGAACAGGTCACCCACACAAAACTTTTAATACATTTGAACTCTATAAAGTTT	1168
981	Db	TATTTTATTCGTTAAATAAATAAATAAATAATTTTAAAAAATAATTTTATACGAAA	922
1169	Qy	CAATGTGAACGTAGACAAGTAACCTCTACTTCC-----CCTTTCTTAACATATCTT	1223
921	Db	ACGACGAAATAATTAATAATAAATAATTAATAATTAACGAAATTTTATACGTAAAAA	862
1224	Qy	TACAAATTAATCAAAATTCGAATTTTAAATAATTCACCTAGTAATAAATAAATTAACATATC	1283
861	Db	AATAAAAAAACGATTTTTTTTAAATAAATAATTTTAAATAATCGTTTATAATTTATTT	802
1284	Qy	AGCTGGGGGAATTTACTAATGATAAAAAAACAACCTGATTTTCAATTTCTCTGTAATAA	1343
801	Db	TAAATATATAATTAATAATAATTTTATTAATTTTAAATTTTAAAAATTAATAAATAA	742
1344	Qy	AGACTGTAACCAATTAATAATCCAAATTTGTTTACCAAGCTATAATAGTTATAGTCATAT	1403
741	Db	ATTATAATAATAAATTAATTTTAAAAATTTTAAATATAAATAAATAAATAAATAAATAA	682
1404	Qy	TTTATCCAGTTTTCTTTTATTTAATTTATCTCTATAAATAATGGAAT-----AGC	1451
681	Db	TATTTTTTTTTTTTTTAAATAAATAATTTATTTTAAAAATAATTTTAAAAAATAATTTA	622
1452	Qy	GCTAAATATATATATACAGGTGCATTTAGGATGGACACACAGTAGTGTTAATAGAAATAA	1511
621	Db	TTTATATAATAATTTTTTTTAAATAATTTATTTAATAATAAATAATTTTAAATAAACCTT	562
1512	Qy	TGCAATATCAGATAAATAATAACATGATCCCGAGCAATCAAGGTAAACAGCTCTGTATAC	1571
561	Db	TATAATA-ATTATATAAATAATTTAATTTTAAATAATAATTTTAAATAATAATAATAAT	503
1572	Qy	AAACTTAAGTAAATTGAGGACCTGGTCATACAGGAGGAACCTGGTTTATTTTACAAG	1631
502	Db	AAATTTTAAATTTTTTTTATTTTAAATAATAATTTTAAAAATAATTTTAAAAATAAT	443

568	C	-----ATTATAATAGATTAAATAAATCTTTATT	CATAGA	600
	Db			
676	Qy	TATAGTAACTATTGTGCAAAATACCTATAGAGAAGGACTTAAATAA	ACTTCGAAAACGAACCT	735
601	Db	TATACGAAACATTTGTTGGACACATACAAATCAAGGATTTAGAAAA	ACTTAAAGAGGTACTAAT	660
736	Qy	AAATAGAGATGGAGTATATTTTAATGATATTCGAAGATATATGACT	TATTTACTGTATTAGAT	795
661	Db	ACTCGAAATGGGCAAGATTCAATCAGTTTAGGAGAGATTTAAACAT	TTTACTGTATTAGAT	720
796	Qy	ACTATCCGCTCAATTTTCTTTTATGATATAAAGAGATA		833
721	Db	ATCGTGTCTCTTTTTCGCAACTACGATGTTAGAACATA		758

RESULT 14
US-09-837-961-7
; Sequence 7, Application US/09837961
; Publication No. US20040058860A1
; GENERAL INFORMATION:

Year	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	Q11	Q12	Q13	Q14	Q15	Q16	Q17	Q18	Q19	Q20	Q21	Q22	Q23	Q24	Q25	Q26	Q27	Q28	Q29	Q30	Q31	Q32	Q33	Q34	Q35	Q36	Q37	Q38	Q39	Q40	Q41	Q42	Q43	Q44	Q45	Q46	Q47	Q48	Q49	Q50	Q51	Q52	Q53	Q54	Q55	Q56	Q57	Q58	Q59	Q60	Q61	Q62	Q63	Q64	Q65	Q66	Q67	Q68	Q69	Q70	Q71	Q72	Q73	Q74	Q75	Q76	Q77	Q78	Q79	Q80	Q81	Q82	Q83	Q84	Q85	Q86	Q87	Q88	Q89	Q90	Q91	Q92	Q93	Q94	Q95	Q96	Q97	Q98	Q99	Q100
1956	TACTTCCTCTGTAGCGCAAAATAGAGAAAAACAAAAATTTAGAACTATCCAAACAAAAT	2015																																																																																																		
Qy																																																																																																				
1993	TTAAAAATTTAATA-----AAATTTTAAATATATTTTAAATTTAAATATATTTTAAATATTT	2048																																																																																																		
Db																																																																																																				
2016	AAATACATTTTTTACCAATCATACAAAAATATCTTTAAATATAGAGCCCAAAACTATGA	2075																																																																																																		
Qy																																																																																																				
2049	---TTTATTTTTTAAAAATTTTATAAAAATATTTTAAATATATATAAATATATATATATAA	2105																																																																																																		
Db																																																																																																				

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RESULT 13
; Sequence 5, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Steلمان, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660

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; PRIOR FILING DATE: 1989-06-27
;
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 3522
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; US-09-837-961-7

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DB	QY
388	ATTTCGATTTTGGCTTAATACAGACGACGCTTTTAATACAGCAATAAAATTTTACACATTACA
496	ACTTATAAAGCGTATTACTACCTATTATTANGCGACGCTGCTAAATTTTCATTTAAATTTTA

448	Db	AGTTTATGAAATCCCTCTTTTATCGGTCTATGTTTCAAGCGCGGAATTTACATTTATACACIA	5
556	Qy	TTACACACAGGTGCTGAATTTGGCTGATGGAATGGAATGCAGATATACATCCTTCACAAATT	615
598	Db	TTAAGAGACGCTGTATCGTTTGGCAGGGTTGGGGACTGATATAGCTACTGTGTTAAATAAT	56
616	Qy	GAACCTAATGCTGGAAACATCAGATGACATATATAAACTTTTAAAGAAGAAATATACCTTAA	675
568	Db	C-----ATTATAATAGATTAATAAATCTTTTATTCATAGA	60
676	Qy	TATAGTAACTATTGCGAAATACCTATAGAGAGGACTAAATAAACTTCGAAACGAAACCT	733
601	Db	TATACGAAACATTGTTTGGACACATACATCAAGGATTAGAAAACCTTAAGAGGTACTAAT	66

Qy	736	AATATGAGATGGAGTATATTTAAATGATTTATCGAAGATATATGACTATTACTGTATTAGAT	795
Db	661	ACTCGAAATGGCGAAGATTCAATCAGTTTAGGAGAGATTTAACTTCTGTATTAGAT	720
Qy	796	ACTATCGCTCAATTTTCTTTTTTATGATATAAAGAGATA	833
Db	721	ATCGTTTGCTCTTTTTCCGAACCTACGATGTTTGAACATA	758

Search completed: February 15, 2006, 05:12:27
Job time : 1555 secs

Qy 796 ACTATCGCTCAATTTCTTTTATGATATAAAGAGATA 833
| | | | | | | | | | | | | | | | | | | | | |
Db 721 ATCGTGTCTTTTTCGAACTACGATGTTAGAACATA 758

RESULT 15
 US-10-825-751-7
 ; Sequence 7, Application US/10825751
 ; Publication No. US20040194165A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Payne, Jewel
 ; APPLICANT: Sick, August J.
 ; TITLE OF INVENTION: Novel Bacillus thuringiensis Isolate Active Against Lepidopteran
 ; TITLE OF INVENTION: Pesces, and Genes Encoding Novel Lepidopteran-Active Toxins
 ; FILE REFERENCE: MA-43CDF2D4
 ; CURRENT APPLICATION NUMBER: US/10/825.751
 ; CURRENT FILING DATE: 2004-04-16
 ; PRIOR APPLICATION NUMBER: US 09/837,961
 ; PRIOR FILING DATE: 2001-04-19
 ; PRIOR APPLICATION NUMBER: US 09/521,344
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: US 08/933,891
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: US 08/356,034
 ; PRIOR FILING DATE: 1994-12-14
 ; PRIOR APPLICATION NUMBER: US 08/210,110
 ; PRIOR FILING DATE: 1994-03-17
 ; PRIOR APPLICATION NUMBER: US 07/865,168
 ; PRIOR FILING DATE: 1992-04-09
 ; PRIOR APPLICATION NUMBER: US 07/451,261
 ; PRIOR FILING DATE: 1989-12-14
 ; PRIOR APPLICATION NUMBER: US 371,955
 ; PRIOR FILING DATE: 1989-06-27
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 7
 ; LENGTH: 3522
 ; TYPE: DNA
 ; ORGANISM: Bacillus thuringiensis
 US-10-825-751-7

Query Match	3.8%;	Score 79.6;	DB 8;	Length 3522;
Best Local Similarity	53.3%;	Pred. No. 0.00024;		
Matches	212;	Conservative 0;	Mismatches 159;	Indels 27; Gaps 1;
Qy	436	ATACGATTTGAGATGTTTCAAAATGATTTTATTCGAGAAATACCTGGTTCCCACTTGAA	495	
Db	388	ATTTCGATTTGCTAATACAGACGCGCTTTAATAACAGCAATAAAATAATTTTACACTTACA	447	
Qy	496	ACTTATAAACGCTATTACTACCTATTATTATGCGCAAGCTGCTAAATTTTCATTTAAATTTA	555	
Db	448	AGTTTTGAAATCCCTCTTTTATCGTCTATGTTTCAAGGGCGAATTTACATTTATCACTA	507	
Qy	556	TTACAACAAGTGCTGTAATGGCTGATGAAATGGAATCGAGATATACATCTCTTCAAAATT	615	
Db	508	TTAAGAGACGCTGTATCGTTTGGCGAGGTTGGGCACTGGGATATAGCTACTGTGTTAAATAA	567	
Qy	616	GAACTAATGCTGGAAATCATCAGATGACTATATATAAACTTTTAAAGAGAAATATACCTTAA	675	
Db	568	C-----ATTATAATAGATTAAATAAACTTTTATTCATAGA	600	
Qy	676	TATAGTAACATTTGCGAAATACCTATAGAGAAGGACTTAATAATAAATTCGAAACGAACTT	735	
Db	601	TATACGAAACATTTGTTGGACACATACAAATCAAGGATTAGAAACTTAAAGAGGTACTAAT	660	
Qy	736	AATATGATGAGGATGATATTTTAATGATTTATCGAAGATATATGACTATTAATCTGTATTAGAT	795	
Db	661	ACTCGACAATGGGCAAGATTTCAATTCAGTTTAGGAGAGATTTAAACACTTACTGTATTAGAT	720	

Result No.	Score	Query Match	Length	DB	ID	Description
1	75.6	3.6	1959	11	US-11-192-801-1	Sequence 1, Appli
2	72.4	3.5	1959	11	US-11-192-801-3	Sequence 3, Appli
C 3	71.8	3.4	171486	11	US-11-121-086-105	Sequence 105, Appl
C 4	71.4	3.4	173602	11	US-11-121-086-25	Sequence 25, Appl
C 5	65.2	3.1	149553	11	US-11-098-686-8738	Sequence 8738, Ap
C 6	65	3.1	139054	11	US-11-121-086-96	Sequence 96, Appl
C 7	63.8	3.1	171486	11	US-11-121-086-105	Sequence 105, App
8	61.8	3.0	173602	11	US-11-121-086-25	Sequence 25, Appl
9	60.8	2.9	139054	11	US-11-121-086-96	Sequence 96, Appl
10	59.4	2.8	158692	11	US-11-121-086-30	Sequence 30, Appl
11	58.6	2.8	2031	11	US-11-058-727-51	Sequence 51, Appl
12	58.6	2.8	2031	11	US-11-058-727-83	Sequence 83, Appl
13	58.6	2.8	2031	11	US-11-108-389-51	Sequence 51, Appl
14	58.6	2.8	2031	11	US-11-108-389-83	Sequence 83, Appl
15	58.6	2.8	2031	11	US-11-224-624-51	Sequence 51, Appl
16	58.6	2.8	2031	11	US-11-224-624-83	Sequence 83, Appl
17	57.4	2.8	2028	11	US-11-058-727-39	Sequence 39, Appl
18	57.4	2.8	2028	11	US-11-058-727-71	Sequence 71, Appl
19	57.4	2.8	2028	11	US-11-108-389-39	Sequence 39, Appl
20	57.4	2.8	2028	11	US-11-108-389-71	Sequence 71, Appl
21	57.4	2.8	2028	11	US-11-224-624-39	Sequence 39, Appl

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QY 618 ACCTAATGCTGGAACATCAGATGACTATTATATAACCTTTTAAAGAAAAATATACCTAAATA 677
Db 660 ATATCTTTCAGAAAGATGTTGCTGAATTTTATCATAGACAAATTAAACTTTTACACACAAATA 719
QY 678 TAGTAACCTATTGTGCAAACTACCTATAGAGAAGGACTAAATAAACTTTCGAAACGAACCTAA 737
Db 720 CACTGACCAATGTGTTAAATGGTATTAATGTTGGATTAAATGGTTTAAAGAGTTCAACTTA 779
QY 738 TAGGAGATGAGTATATTTAATGAATTCGAAGATATATGACTATTAATGCTATTAAGATAC 797
Db 780 TGATGCATGGTCAAATTTAAACCGTTTTCGCAGAGAAATGACTTTAACTGTATTAGATCT 839
QY 798 TATCGCTCAATTTCTTTTATGATATATAAGAGATACAAGA 839
Db 840 AATTGTAATTTTCCCATTTTATGATATTCGGTTATATCTCAA 881

RESULT 2
US-11-192-801-3
; Sequence 3, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; PRIOR FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1959
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1956)
; OTHER INFORMATION: naturally occurring nucleotide sequence encoding a
; CRY3Bb2 amino acid sequence
US-11-192-801-3

Query Match 3.5%; Score 72.4; DB 11; Length 1959;
Best Local Similarity 52.0%; Pred. No. 3.8e-05;
Matches 209; Conservative 0; Mismatches 166; Indels 27; Gaps 1;

QY 438 ACGATTTGAGATGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAC 497
Db 507 ACTTTTCTCAAGCAGAAAGTCATTTTCGTAAATCCATGCCGTCAATTTGCGAGTTTCCAA 566
QY 498 TTATAAAACGCTATTACTACCTATTATGCGCAAGCTGCTAAATTTTCATTTTAAATTTATT 557
Db 567 ATTGGAAGTGTGTTTCTACCAACATATGCAAGCTGCAATATACATTTATTGCTATT 626
QY 558 ACAACAAGGTGCTGAATTGGCTGATGAATGGAATGCAGATATACAPCTTCAAAATGA 617
Db 627 AAAAGATGCTCAAGTTTTTGGAGAAAGATGG-----GG 659
QY 618 ACCTAATGCTGGACATCAGATGACTATTATATAACTTTTAAAGAAAAATATACCTAAATA 677
Db 660 ATATCTTTCAGAAAGATGTTGCTGAATTTTATCATAGACAAATTTAAACTTTACGCAACAAATA 719
QY 678 TAGTAACCTATTGTGCAAACTACCTATAGAGAAGGACTAAATAAACTTTCGAAACGAACCTAA 737
Db 720 CACTGACCAATGTGCTCAATTTGTTAATGTTGGATTAAATGGTTTAAAGAGTTCAACTTA 779
QY 738 TAGGAGATGAGTATATTTAATGAATTCGAAGATATATGACTATTAATGCTATTAAGATAC 797
Db 780 TGATGCATGGTCAAATTTAAACCGTTTTCGCAGAGAAATGACTTTAACTGTATTAGATCT 839
QY 798 TATCGCTCAATTTCTTTTATGATATATAAGAGATACAAGA 839
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Db 840 AATTGTAATTTTCCCATTTTATGATGTTCCGGTTATATCTCAA 881

RESULT 3
US-11-121-086-105/c
; Sequence 105, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 105
; LENGTH: 171486
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-105

Query Match 3.4%; Score 71.8; DB 11; Length 171486;
Best Local Similarity 44.1%; Pred. No. 9.1e-05;
Matches 580; Conservative 0; Mismatches 717; Indels 18; Gaps 6;

QY 775 ATGACTATTACTGTATTAGATACTATCGCTCAATTTTCTTTTATGATATAAGAGATAC 834
Db 17682 ATCTATAATATAATAATATAATAATATATTTATATATCTCTATAATATAATAATATAA 17623
QY 835 AAAGATTCAATAGGAAGATAGGTGGCATTA-ACCTGAACCTTACAAGAGAAATTTATAC 893
Db 17622 ATATATTTATATATCTATATAATATAATAATATATTTATATATCTATAATATAATAA 17563
QY 894 AACTGAAATAAATTTTGACCGCTTACTTACCTTGAATTTCAACCCCACTCGCTATAAT 953
Db 17562 ATCTATAATATAATTTATATATATCTATAATAATAATAATCTATAATAATATTTATATA 17503
QY 954 GGAATATAATTTAAACACGTTACGGGCTTAGAGATTATTTTCATTTTATAGATGAACCTTAT 1013
Db 17502 TCTATAATATAAA-----ATCTATAAATAATATTTATATATATCTATAATAATAAT 17450
QY 1014 TTATACAAAAAATGAAACGTCAGGGAATCGTTTGTGTTGTAATTCGGAATCGTAATAGATC 1073
Db 17449 CTATAAATAATTTATATATATCTATAATAATAATACTATAATAATATTTATATATATC 17390
QY 1074 TACTTATGCTAGCAGCAAGAACTGAAATTTATATATCGAGAGAAACACAGGTCCACCCACAAC 1133
Db 17389 TATAATATAATAAATCTATAAATAATATTTATATATCTATAATAATAATAATAATAATA 17330
QY 1134 AAAAATTTTAAATACCATTTGAATCCTATAAAAGTTTCAATTTGTAACCTGATAGACAAGTAAC 1193
Db 17329 TATTTATATATCAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 17270
QY 1194 TCCTACTTCCCTTTTCCCTAACATATCTTTACAAATTAATCAAAATGGAACCTTTATTTAAA 1253
Db 17269 AAATATAATAATATATTTTATATATCTATAATAATAATAATAATAATAATAATAATAATA 17210
QY 1254 TAATTCACCTAGTATAAATAAACAATNTTCAGCTGGGGGAATTTTCTCTAAATGATAAAAA 1313
Db 17209 TCTATAAATATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 17150
QY 1314 AACAACTGATTTTCAATTTTCCGTAAAAAAGAGCTGTAAACCAATTTTAAATCCCAAAATG 1373
Db 17149 TATATTTATATATCTATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 17094
QY 1374 TTTACCAAGCTATAATAGTTATAGTCATATTTTATCCAGTTTCTTTTAAATTTATTC 1433
Db 17093 TATAATAATATAAAATTTTATATATATCTATAATAATAATAATAATAATAATAATAATAATA 17034
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1434	CTATAAAATTGGATTAGCCTAAATATATATATACAGGTGCAATTAGGATGGACACACAG	1493	QY
17033	CATATATAAATACAAAATATATATCTCATATAAAATATACAAATATATTTATATAT	16974	Db
1494	TAGTGTTAATAGNAATAATGCAATATACAGATAAAATAATTTACAATGATCCACGAATCAA	1553	QY
16973	ATCTATCATATATAAAATATACAAATATATTTATATATCTCATATATAAATATACAA	16914	Db
1554	AGGTAACAGCTCTTGATACAAACTCTAAGGTAAATTGAAGGACCTGGTCATACAGGAGGAAA	1613	QY
16913	ATATATTTATATAATCTATCATATATAATATAATAAATGTTATTTATATAAAATATATAA	16854	Db
1614	CTTGGTTTATTTACAAGTCAGGGGTTTAGAGATTACATGTAGAACTCCTAATTTCTAC	1673	QY
16853	TATATTTATATTTATAGATAAATATATGTTATTTCTATAATTTATATAATAATTTATAT	16794	Db
1674	ACAATCTTATTACATTTAGACTTCGATACGCTACAAATGGTGTGGAAATACTCTTCCTAA	1733	QY
16793	AATATGTAATGTTATATATGTTATATATTTAAGACATATAATAATATATTTAATTTAA	16734	Db
1734	TATATCTCT - TACAATACAGGAGTAATAGGAATACCACCTCAACGACTCAACAACACT	1791	QY
16733	TATATTTATATAATAATATTTATTAATATATTTTATATAAATTTAATATATTTATTA	16674	Db
1792	TTTTCTGGTACAAATTTATATAATTTTACATACGAGATTTTGGGTATTTCCAAATTTCCA	1851	QY
16673	TATTAATATGTAATATTTATCTCATATAATAAATATATATTAATTTTAAATATAT	16614	Db
1852	AGTACAGTAACATTACCTTTAAATCGAAACATACCATTATTTAATCGTGC - GAGT	1910	QY
16613	TATATAATAATATAATATTTATATAAAATATATAATATAATACATAATATTTATAT	16554	Db
1911	ATCAAAATTCAAATTTAATCATTTGATAAAATTTGAATTTATACCAATTACTTCCCTGTACG	1970	QY
16553	ATTATGTTATATATATTTATATTTGTTTAAATTTATTTAATAATAATTTAATATGTA	16494	Db
1971	CCAAATAGAGA - - AAAACAAAAATTTAGAAACTATCCAAACAAAAATAATACATTTTT	2027	QY
16493	ATATAATTTATATAATATAAATCTTTATATAATTTTATATATTTATATAATAATTA	16434	Db
2028	CACAAATCATACAAAAAATCTTTAAATATAGAACCCACAAACTATGATATGTAT	2082	QY
16433	TAAATATATATATTTATATAATTTATAAATATAAATATCAAAATTTATATATATTAAT	16379	Db

RESULT 4
 US-11-121-086-25/c
 ; Sequence 25, Application US/11121086
 ; Publication No. US20050266459A1
 ; GENERAL INFORMATION:
 ; APPLICANT: POULSEN, TIM S.
 ; APPLICANT: NIELSEN, KIRSTEN V.
 ; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
 ; FILE REFERENCE: 09138.6000-00000
 ; CURRENT APPLICATION NUMBER: US/11/121,086
 ; CURRENT FILING DATE: 2005-05-04
 ; PRIOR APPLICATION NUMBER: 60/567,570
 ; PRIOR FILING DATE: 2004-05-04
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 25
 ; LENGTH: 173602
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-121-086-25

	Query Match	3.4%	Score 71.4;	DB 11;	Length 173602;
	Best Local Similarity	42.5%;	Pred.No. 0.00011;		
	Matches 551; Conservative	0;	Mismatches 736;	Indels 8;	Gaps 3;
Qy	737 ATATGAGATGGAGTGATATTTTAATGATTATCGAAGATATATGACTATTACTGATTAGATA 796				
Db	137315 ATATGAATT 137256				

Qy	797	CTATCGCTCAATTTTCTTTTTATGATATAAGAGATACAAAGATTCCAATAGGAAGATAG	856
Db	137255	ATATTTATATTTTATATATACATATTTATATATATATATATATATATATATATATATAT	137196
Qy	857	GTGGCATTAAACCTGAACCTTACAAGAGAAATTTATACAACCTGAAATAAAATTTTGACCGCTC	916
Db	137195	ATATAATATATGAT	137136
Qy	917	TTACTTACCTTGGAAATTCACACCCAAATCTCGCTATAAATGGAATATAATTTTAACACGTTCCAG	976
Db	137135	ATAATTTATATACAT	137076
Qy	977	GGCTTAGATTATTTTCATTTTATAGTGAACCTTATATTTTATACAAAAAATGAAACGTACG	1036
Db	137075	GTATATAAATTTATATAAT	137016
Qy	1037	GGAACTCGTTAGTTGGTATTTGCGAATCGTAATAGATCTACTTATGCTACGACAGCAACTG	1096
Db	137015	ATATATATATATATATAAT	136956
Qy	1097	AAATTTATATATGGAAGAAAGACAGGCTCCACCCACAACAAAAAATTTTAAATACCATTTGAAT	1156
Db	136955	TAATAATATATAAATATATATATATATATATATATATAAACAATTTATATAAATATATTATA	136896
Qy	1157	CCTATAAAGTTTCAA--TTGTAACGTGATGACAGTAACCTCTACTCTCCCTTTTCCCTAAC	1215
Db	136895	TATATAATATAAACAATTTATATAAATATATATATATATATATATAAACAATATATATAA	136836
Qy	1216	ATATACCTTACAATTAATCAAAATTTGAACCTTTATTTTAAATATTCACCTAGTAATAAATTA	1275
Db	136835	ATATAAATATATAAACAATTTATATAAATATAAATATAAATATAAACAATATATATAAAT	136776
Qy	1276	ACATATTCAGCTGGGGGAAATTTATCTAAATGATAAAAAAACAACCTGATTTTCAATTTCCCT	1335
Db	136775	ATAATAATATAAACAATTTATATAAATATAAATATAAATATAAATATAAATATAAATATA	136716
Qy	1336	GTAAAAAAGACTGTAACCAATTTATTAATCCAAATTTGTTTACCAGCTATAAATAGTTAT	1395
Db	136715	TAATATATAAATATATTTATATAAATATACTATATAAATATAGCATATAAATATAAATAA	136656
Qy	1396	AGTCATATTTTATCCGAGTTTTCCTTATTTAAATTTTCTTATAAATTTGGATTTAGCGCTA	1455
Db	136655	TATATTATATAAAAAATATAAACAATTTATATAAANAATTTATAAANAATATAAATATAA	136596
Qy	1456	AAATATTTATATACAGGTGCATTTAGGATGGACACACAGTAGTGTGTTAAATAGAAAAATGCA	1515
Db	136595	AAATATTTTATATATATATATTTATATATACATTAACAATATAAATATAAATATATACT	136536
Qy	1516	ATATCAGATAAAAAATATACAAATGATCCAGCAATCAAAGGTAAACAGCTTGTGATACAAC	1575
Db	136535	ATATAAATATATATAAATATATAAATATATAAATATATATATATTTATAAATATAGTATATAT	136476
Qy	1576	TCTAAGGTAAATGAAGGACCTGGTCATACAGAGGAAACTTTGGTTTATTTTACAAAGTCNA	1635
Db	136475	TTATATAGATTTTATATAAATTTATATATATTTTATATATATAAATTTTATATATATTT	136416
Qy	1636	GGCGGTTTTAGAGATTTACATGTAGAACCTCTAATTTCTACACAATCTTATTACATTTAGACTT	1695
Db	136415	TATATATTTTATATATAAATTTTATATATATTTTATATATATATAAATTTATATATTTGAT	136356
Qy	1696	CGATACGCTACAAA-----TGGTGCTGGAAATACTCTTCCTTAATATATATCTCTTACAATA	1749
Db	136355	ATAATTTATATAAATAATATAAATTTTATATATAAATATAAATAAATTTATATATATATATAT	136296
Qy	1750	CCAGGAGTAATAGGAATACCACTCAACGACTCAACAACACTTTTCTGGTACAAATTTAT	1809
Db	136295	TTATATATTTATATAAATAATATAAATTTTATATAAATTTTATATATATATAAATATATAT	136236
Qy	1810	AATAATTTTACAATACGGAGATTTTGGGTATTTTCCAAATTTTCCAAGTACAGTACAAATTCCT	1869
Db	136235	ATPAATTTTATATATTTTATATAAATATAATATAATTTTATATAAATATAAATATAATTTAT	136176

QY 1297 TTATCTAATGATATAAAACAACTGATTTTCATTTTCCTGTAAAAAGAGCTGTAAACCA 1356
DB 17348 TTATAGATATATATAAATATATTTATAGATTTATATATATTATAGATATATA--TAAATATA 17405
QY 1357 ATTATTAATCCAAATTTGTACCACAGCTAATAAGTATAGTCATATTTATCCCAAGTTT 1416
DB 17406 TTTATAGATTTATATATTATAGATATATATAAATATATTTATAGATTTATATATAGA 17465
QY 1417 TCTTTATTTAAATTTCTCTATATAAAATGGATTTAGCGCTAAATATA 1461
DB 17466 TATATATAAATATATTTATAGATTTATATATATTATAGATATATA 17510
RESULT 8
US-11-121-086-25
; Sequence 25, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 173602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-25

Query Match 3.0%; Score 61.8; DB 11; Length 173602;
Best Local Similarity 44.5%; Pred. No. 0.0075;
Matches 462; Conservative 0; Mismatches 567; Indels 10; Gaps 5;
QY 432 TAAATPACGATTTGAGAATGTTCCAAATGATTTTATTCGAGAAATACCTGGTTTCCAAT 491
DB 136072 TAATATATATATAAATATATATGTTATATATTTTATATATAAATATATATATATAT 136131
QY 492 TGAACCTTTAAACCGCTTACTACTCTATTTATGCGCAAGCTGCTAAATTTTCATTAA 551
DB 136132 ATAAATATATAAATATATAATATATATATATATATATATAAATATAAATATATATA 136191
QY 552 TTATTACCAACAGGTGCTGAATGGCTGATGAATGGAATGCAGATATACATCCTTCACA 611
DB 136192 TATATAAATATATAATATATATATATATAAATATATAAATATATATATATATATAA 136251
QY 612 AATTGAACCTTAATGCTGGCAATCAGATGACTATTTATAAATTTTAAAAAGAAATATACC 671
DB 136252 TATATAAATATATAAATATATATATATATATATAAATATATAAATATATAAATATA 136311
QY 672 TAAATATAGTAATTTGTCGAATACCTATAGAGAGAGACTTAATAAATCGGAACCA 731
DB 136312 TAAATATATATATAAATATATAAATATATATATTTTATATAAATATATAAATATA 136371
QY 732 ACTTAATATGAGATGAGTATATTTTAAATGATTCGAAGATATATGACTATTACTGTATT 791
DB 136372 TTATATATAAATATATAAATATATAAATATATAAATATATAAATATATAAATATA 136430
QY 792 AGATACCTGCGCTCAATTTCTTTTATGATATAAAGAGATCAAAAGATTCATATAGGAAG 851
DB 136431 ATATAAATATATAAATATATAAATATATAAATCTATATAAATATATAAATATATA 136490
QY 852 AATAGTGGCAT--TAAACACCTTACAGAGAAATTTTACAACTGGAATAAATTT 908
DB 136491 TAAATATAGTATATATTTATATATATTTTATAAATATTTTATATAGTATATATATA 136550
QY 909 TGACCGCTTTACTTACCTTGAATTTCAACCCCAATCTCGCTATAAATGGAATATAAATTTAAC 968
DB 136551 TTTATATGTTATGATATAAATATATAAATATATAAATATATTTATATATATATATTT 136610

QY 969 ACGTTCAGGGCTTAGATTTATTTTCATTTTATAGTGAAGTATATTTTATACAAAAAATGA 1028
DB 136611 TATATAAATATTTTATATAAATATGTTATATATTTTATATAAATATATATATATATA 136670
QY 1029 AACGTACGGGAATCGTTAGTTGGTATTCGGAATCGTAATAGATCTACTTATGCTACGAC 1088
DB 136671 TCGTATATATATAGTATATATATATAAATATTTTATATATATATATATATATATAT 136730
QY 1089 AGGAACCTGAAATTTATATATGGAGAAAGAACACAGGTCACCCACAAACAAACCTTTAATACC 1148
DB 136731 A-ATATTTATATATATATTTTATAAATATGTTTATATATATTTATATATATAA-T 136788
QY 1149 ATTTGAATCCCTATAAAGTTTCAATTTGTAACCTGATAGACAAGTAACCTTCCCTTT 1208
DB 136789 GTTTATATATTTATATATTTTATATAATATGTTTATATATATTTATATATAATATGT 136848
QY 1209 TCCTAACATATATCTTTACAAATTAATCAAAATGAACTTTTATTTAAATAAATTCACCTAGTAA 1268
DB 136849 TTATAATATATAATATATATTTTATATAATGTTTATATATATATATATAATATTTTA 136908
QY 1269 TAAATTAACATATTCAGCTGGGGGAAATTTATCTAATGATAAAAAACAACCTGATTTTCA 1328
DB 136909 TATAATATGTTTATATATATATATAAATATATTTATATATATTTATATATATTTATA 136968
QY 1329 ATTTCTGTAAAAAAGACTGTAAACCAATTTAATCCAAATTTGTTTACCAGCTATAA 1388
DB 136969 ATAT----ATAATATATAAATATAAATATAATATATATATATATATATATATATAT 137024
QY 1389 TAGTTATAGTCATATTTTATCCAGTTCCTTTTAAATTTTCTTTTAAATTTTCTATAAAATTCGATT 1448
DB 137025 TAGTTATATAAATATAAATATAATATATGTTATATAATTTATATAACATATATATAT 137084
QY 1449 ACGCGTAAATATATATAT 1467
DB 137085 ATGTATATAAATATATAAT 137103

RESULT 9
US-11-121-086-96
; Sequence 96, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 96
; LENGTH: 139054
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-96

Query Match 2.9%; Score 60.8; DB 11; Length 139054;
Best Local Similarity 45.7%; Pred. No. 0.011;
Matches 406; Conservative 0; Mismatches 467; Indels 15; Gaps 5;
QY 584 AATGGAATGCAGATATACATCCTTCACAAATTTGAACCTTAATGCTGGAACATCAGATGACT 643
DB 43306 AATATAAATAAATATATTTTACTATTAAATAAATAAATAATATATATATATATATAT 43365
QY 644 ATTATAAATTTTAAAGAAATATACCTTAATATAGTAACCTATTGTCGAAATACCTATA 703
DB 43366 ATTATAAATAAATTTTCATAATTTTAAATTTAAATTTAAATTTAAATTTAAATGTA 43425
QY 704 GAGAAAGGACTAAATAAACTTCGAAACGAACTTAATATGAGATGGAGTATATTTAATGATT 763


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; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 2031
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2031)
;
US-11-058-727-51

Query Match      2.8%; Score 58.6; DB 11; Length 2031;
Best Local Similarity 46.9%; Pred. No. 0.017;
Matches 291; Conservative 0; Mismatches 294; Indels 36; Gaps 2;

QY 214 GACAAACAGTATGGACACAATTTTATAAATGGGAGAAATTTTGTGTATACACCGTTA 273
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
322 GAAAGAGTCAATGGGAAATTTTATGGACAAAGTAGAAGAACTCAATTAATCAAAAAATA 381
QY 274 ACAGAAAGCATAAACAGCTAAAGTTACAACTTTTAGAAGGATTTAGACAAATATTACAA 333
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
382 GCAGAAATATGCAAGGAATTAAGCGCTTCGGAATTTAGAGGATTAGGTAAATATTACCAA 441
QY 334 AGCTATAATACAGCATTTAGATGATTTGAGAAAAATTTAAAGAGCTACAAGCTCTCGATT 393
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
442 TTATATCTAATCGCTTGAAGATGGGAGAAATCCATTTTGAAGTCGAGGTAGTTTA 501
QY 394 CCACCATCATCAGATTACAAAGCTGCTTGAATCTTAAATACGATTTGAGATGTT 453
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
502 AATGTTCCCGGCAGCTTACGAGATG-----TGCAGAAATCGATTTGAAATCCTG 552
QY 454 CACAATGATTTTATTCGAGAAATACCTGTTTCCAACTTTGAAACTTTATAAAACGCTATTA 513
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
553 GATAGTTTATTCGCAATATATGCCATCTTTTAGTGACAAATTTTGAAGTACCATTC 612
QY 514 CTACCTATTATTCGCAAGCTGCTAATTTTCAATTTTAAATTTATTATTAACAAGTGTGAA 573
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
613 CTTACTGTATATGCAATGGCAGCAACCTTCACTTTACTGTATTAAGGCGGTCAATT 672
QY 574 TTGGCTGATGAATGGAATGCAGATATACATCTTCAAAATTTGAACCTAATGCTGGAACA 633
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
673 TTTGGAGAGAAATGGGGATGGTCAACAACCT-----ACT 705
QY 634 TCAGATGACTATTATAAACTTTTAAAGAAATATACCTAAATATAGTAATCTTGCA 693
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
706 ATTAATAACTATTATGATCGTCAAAATGAAACTTACTGCGAGAAATATCTGTATCTGTGA 765
QY 694 AATACCTATAGAGAAGGACTTAAATAAATTCGAAACGAACTAATATGAGATCGAGATTA 753
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
766 AAGTGGTATGAACTGTTTAGCAAAATTTAAAGGACGAGCGCTAAACAAATGGGTGAC 825
QY 754 TTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACTATCGCTCAATTTCT 813
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
826 TATAACCAATTCGATAGAGAAATGACACTGGCGGTTTTAGATGTTGTTGATTTATTCCTCA 885
QY 814 TTTTATGATATAAGATAC 834
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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DB 886 AATTATGACACACGACGCTAC 906

RESULT 12
US-11-058-727-83
; Sequence 83, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 2031
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2031)
;
US-11-058-727-83

Query Match      2.8%; Score 58.6; DB 11; Length 2031;
Best Local Similarity 46.9%; Pred. No. 0.017;
Matches 291; Conservative 0; Mismatches 294; Indels 36; Gaps 2;

QY 214 GACAAACAGTATGGACACAATTTTATAAATGGGAGAAATTTTGTGTATACACCGTTA 273
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
322 GAAAGAGTCAATGGGAAATTTTATGGAAACAGTAGAAGAACTCAATTAATCAAAAAATA 381
QY 274 ACAGAAAGCATAAACAGCTAAAGTTACAACTTTTAGAAGGATTTAGACAAATATTACAA 333
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
382 GCAGAAATATGCAAGGAATTAAGCGCTTTCCGGAATTTAGAGGATTAGGTAAATATTACCAA 441
QY 334 AGCTATAATACAGCATTTAGATGATTTGAGAAAAATTTAAAGAGCTACAAGCTCTCGATT 393
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
442 TTATATCTAATCGCTTGAAGATGGGAGAAATCCATTTTGAAGTCGAGGTAGTTTA 501
QY 394 CCACCATCATCAGATTACAAAGCTGCTTGAATCTTAAATACGATTTGAGATGTT 453
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
502 AATGTTCCCGGCAGCTTACGAGATG-----TGCAGAAATCGATTTGAAATCCTG 552
QY 454 CACAATGATTTTATTCGAGAAATACCTGTTTCCAACTTTGAAACTTTATAAAACGCTATTA 513
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
553 GATAGTTTATTCGCAATATATGCCATCTTTTAGTGACAAATTTTGAAGTACCATTC 612
QY 514 CTACCTATTATTCGCAAGCTGCTAATTTTCAATTTTAAATTTATTATTAACAAGTGTGAA 573
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
613 CTTACTGTATATGCAATGGCAGCAACCTTCACTTTACTGTATTAAGGAGCGGTCAATT 672
QY 574 TTGGCTGATGAATGGAATGCAGATATACATCTTCAAAATTTGAACCTAATGCTGGAACA 633
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
673 TTTGGAGAGAAATGGGGATGGTCAACAACCT-----ACT 705
QY 634 TCAGATGACTATTATAAACTTTTAAAGAAATATACCTAAATATAGTAATCTTGCA 693
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 706 ATTAATAACTATTATGATCGTCAAAATGAACTTTACTGCGAGATATTTCTGATCACTGTGTA 765
Qy 694 ATACCTATAGAGAAGGACTAAATAAATCTCGAAGCAACCTTAATATGATGAGTGGAGTATA 753
Db 766 AAGTGTATGAAACTGTTTATGCAAAATTTAAAGAGGACGAGCGCTTAAACAATGGGTGAC 825
Qy 754 TTTAAATGATTATCGAAGATATATGACTATTACTGTATTAGATCTATCGCTCAATTTTCT 813
Db 826 TATAACCAATTCGTAGAGAAATGACACTGGCGGTTTATGATGTTTGTGCAATTATCCCA 885
Qy 814 TTTTATGATATAAGAGATAC 834
Db 886 AATTATGACACGACGCTAC 906
RESULT 13
US-11-108-389-51
; Sequence 51, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 2031
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2031)
US-11-108-389-51
Query Match 2.8%; Score 58.6; DB 11; Length 2031;
Best Local Similarity 46.9%; Pred. No. 0.017;
Matches 291; Conservative 0; Mismatches 294; Indels 36; Gaps 2;
Qy 214 GACAAAACAGTATGAGACAAATTTTAAATGGGAGAAATTTTGTGTACACCGTTA 273
Db 322 GAAAAGAGTCAATGGGAAATTTTATGGAACAAGTAGAAGAACTCATTAATCAAAAAATA 381
Qy 274 ACAGAAAGCATTAACAGCTAAAGTTTAAAGGATTTAGACAAATATTACAA 333
Db 382 GCAGAAATGACAGGAATAAAGCGCTTTCGGAATTTAGAGGATTTAGTAAATACCAA 441
Qy 334 AGCTATAATACAGCAATTAGATGATTGGAGAAAATTTAAAGAGACTACAGCTCCGGAATTA 393
Db 442 TTATATCTAATCGCTTGAAGATGGGAGAAAATCCATTTCCGAAGTCGAGGTAGTTTA 501
Qy 394 CCACCATCATCAGCAATTAACAAGCTCGCTTGACTCTTAAATAACGATTTGAGAAATGTT 453
Db 502 AATGGTCCCGCGCAGCCCTTACGAGATG-----TGCAGAAATCGATTTGAAATCCTG 552
Qy 454 CACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACTTAAATCTTAAACCGCTATTA 513

Db 553 GATAGTTTATTACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCATTTC 612
Qy 514 CTACCTATTATTATGCGCAAGCTCTAATTTTCAATTTTAAATTTTATTAACAAGTGTCTGAA 573
Db 613 CTTACTGTATATGCAATGCGCAGCAACCTTCATTTACTGTTTATTAAGCGCGTCAATT 672
Qy 574 TTGGCTGATGAATGGAATGCAAGATATACATCTTCAAAATTTGAACCTAATGCTGGAACA 633
Db 673 TTGGGAGAAATGGGAGTGGTCAACAACT-----ACT 705
Qy 634 TCGATGACTATTATATAAATCTTTTAAAGAAAATATACCTAAATATAGTAACTATTGTGCA 693
Db 706 ATTAATAACTATTATGATCGTCAAAATGAACTTATCTGCAAGATATTCTGATCACTGTGTA 765
Qy 694 AATACCTATAGAGAAGGACTTAAATAAATCTCGAAGCAACCTTAATATGATGAGTGGAGTATA 753
Db 766 AAGTGTATGAACTGTTTATGCAAAATTTAAAGGACGAGCGCTTAAACAATGGGTGAC 825
Qy 754 TTTAAATGATTATCGAAGATATATGACTATTACTGTATTAGATCTATCGCTCAATTTTCT 813
Db 826 TATAACCAATTCGTAGAGAAATGACACTGGCGGTTTATGATGTTTGTGCAATTATTCCTCA 885
Qy 814 TTTTATGATATAAGAGATAC 834
Db 886 AATTATGACACGACGCTAC 906
RESULT 14
US-11-108-389-83
; Sequence 83, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 2031
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2031)
US-11-108-389-83
Query Match 2.8%; Score 58.6; DB 11; Length 2031;
Best Local Similarity 46.9%; Pred. No. 0.017;
Matches 291; Conservative 0; Mismatches 294; Indels 36; Gaps 2;
Qy 214 GACAAAACAGTATGAGACAAATTTTAAATGGGAGAAATTTTGTGTACACCGTTA 273
Db 322 GAAAAGAGTCAATGGGAAATTTTATGGAACAAGTAGAAGAACTCATTAATCAAAAAATA 381
Qy 274 ACAGAAAGCATTAACAGCTAAAGTTTAAAGGATTTAGACAAATATTACAA 333

Db 382 GCAGAAATATGCAAGGAATTAAGCGCTTTCGGAAATTAGAGGATTAGTGAATTAATACCAC 441
Qy 334 AGCTATAATACAGCATTTAGATGATGGAGAAAATTTAAAGAGCTCAAGCTCCTGGATTA 393
Db 442 TTATATCTAATCTCGCTTGAAGAAATGGGAAGAAATCCATTTTGAAGTGGAGTACTTTA 501
Qy 394 CCACCATCATCAGCATATACACAGCTGCTTGAACCTTTAAATAGATGATGATGATGAT 453
Db 502 AATGGTTCGCGGCGAGCTTTACAGATG-----TGCAGAAATCGATTTGAAATCCTG 552
Qy 454 CACAATGATTTTATTCGAGAAATACCTGTTTCCAACTTTGAAATTTATATAAAGCGCTATTA 513
Db 553 GATAGTTTATACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCATTC 612
Qy 514 CTACCTATTATTCGCGAAGCTGCTAAATTTTCAATTTTAAATTTTATTAACAACAGGTGCTGAA 573
Db 613 CTTACTGTATATGCAATGCGAGCAACCTTCATTTACTGTTATTAAGAGCGGCTCAATT 672
Qy 574 TTGGCTGATGAATGGAATGCGAGATATACATCTCTTCAAAATTTGAACCTTAATGCTGGAACA 633
Db 673 TTTGGAGAAGAAATGGGATGGTCAACAACCT-----ACT 705
Qy 634 TCAGATGACTATTATTAACCTTTTAAAGAAAATATACCTAAATATAGTAATCTGTCGA 693
Db 706 ATTAATACTATTATGATGCTCAATGAACTTCTGCGAATATTTCTGATCACTGTGTA 765
Qy 694 AATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACTTAATATGAGATGGAGTATA 753
Db 766 AAGTGTATGMAACTGGTTTAGCAAAATTTAAAGGCGAGCGCTAAACAATGGGTTGAC 825
Qy 754 TTTAATGATTCGAAGATATATGACTATTAATGATATGATGATGATGATGATGATGATGAT 813
Db 826 TATAACCAATTCGCTAGAGAAATGACACTGGCGGTTTATGATGTTTGTGCAATTAATCCCA 885
Qy 814 TTTTATGATATAAGAGATAC 834
Db 886 AATTATGACACAGCAGCTAC 906

RESULT 15
US-11-224-624-51
; Sequence 51, Application US/11224624
; Publication No. US20060021096A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Andre
; APPLICANT: Dong, Hua
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Rice, Janet
; APPLICANT: Schepers, Eric
; APPLICANT: Wong, James
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/297402
; CURRENT APPLICATION NUMBER: US/11/224,624
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: 10/746,914
; PRIOR FILING DATE: 2003-12-24
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 2031
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS

; LOCATION: (1)....(2031)
US-11-224-624-51
Query Match 2.8%; Score 58.6; DB 11; Length 2031;
Best Local Similarity 46.9%; Pred. No. 0.017;
Matches 291; Conservative 0; Mismatches 294; Indels 36; Gaps 2;
Qy 214 GACAAAACGATATGACACAAATTTTAAATGGGAGAAATTTTGTGATACACCGTTA 273
Db 322 GAAAAGAGTCAATGGGAAATTTTATGGAAACAGTAGAAGAACTCATTAATCAAAAAATA 381
Qy 274 ACAGAAAGCATAAAAACAGCTAAAGTTTACAACTTTTAGAGAGGATTTAGACAAAATATTACAA 333
Db 382 GCAGATATGCAAGGAATTAAGCGCTTTCCGAAATTAGAAGGATTAGTGAATTAATTAACCAA 441
Qy 334 ACCTATAATACAGCATTTAGATGATTTGGAGAAAATTTAAAGAACTCAAGCTCCTGGATTA 393
Db 442 TTATATCTAATCTCGCTTGAAGAAATGGGAAGAAATCCATTTTGAAGTGGAGTACTTTA 501
Qy 394 CCACCATCATCAGATTTACAAACAGCTGCTTGAACCTTTAAATAGATGATGATGATGATGAT 453
Db 502 AATGGTTCGCGGCGAGCTTTACAGATG-----TGCAGAAATCGATTTGAAATCCTG 552
Qy 454 CACAATGATTTTATTCGAGAAATACCTGTTTCCAACTTTGAACTTATAAAGCGCTATTA 513
Db 553 GATAGTTTATTCGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCATTC 612
Qy 514 CTACCTATTATTCGCGAAGCTGCTAAATTTTCAATTTTAAATTTTATTAACAACAGGTGCTGAA 573
Db 613 CTTACTGTATATGCAATGCGAGCAACCTTCATTTACTGTTATTAAGAGCGGCTCAATT 672
Qy 574 TTGGCTGATGAATGGAATGCGAGATATACATCTCTTCAAAATTTGAACCTTAATGCTGGAACA 633
Db 673 TTTGGAGAAGAAATGGGATGGTCAACAACCT-----ACT 705
Qy 634 TCAGATGACTATTATTAACCTTTTAAAGAAAATATACCTAAATATAGTAATCTGTCGA 693
Db 706 ATTAATACTATTATGATGCTCAATGAACTTCTGCGAATATTTCTGATCACTGTGTA 765
Qy 694 AATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACTTAATATGAGATGGAGTATA 753
Db 766 AAGTGTATGMAACTGGTTTAGCAAAATTTAAAGGCGAGCGCTAAACAATGGGTTGAC 825
Qy 754 TTTAATGATTCGAAGATATATGACTATTAATGATATGATGATGATGATGATGATGATGATGAT 813
Db 826 TATAACCAATTCGCTAGAGAAATGACACTGGCGGTTTATGATGTTTGTGCAATTAATCCCA 885
Qy 814 TTTTATGATATAAGAGATAC 834
Db 886 AATTATGACACAGCAGCTAC 906
Search completed: February 15, 2006, 03:05:11
Job time : 434 secs